Figure 1a

	MS-GPC-8-27-7	MS-GPC-8-27-10	MS-GPC-8-6-13	MS-GPC-8-27-41	MS-GPC-8-6-47	MS-GPC-8-10-57	MS-GPC-8-6-27	MS-GPC-8	MS-GPC-8-6
Plastic	-0.004	-0.020	-0.022	-0.025	-0.001	0.005	0.007	-0.022	-0.018
BSA	-0.003	-0.019	-0.021	-0.022	0.008	0.003	0.003	-0.016	-0.019
Testosterone-BSA	-0.005	-0.010	-0.012	-0.007	0.011	0.003	0.002	-0.009	-0.012
Lysozyme	-0.005	-0.079	-0.079	-0.073	0.013	0.014	0.006	-0.081	-0.072
human Apotransferrin	-0.009	-0.016	-0.018	-0.018	-0.005	-0.008	-0.004	-0.014	-0.016
MHCII (DRA*0101/ DRB1*0401)	1.549	1.493	1.467	1.525	1.400	1.256	1.297	1.058	1.306

Figure 1c

Target Proteins	scFv												IgG		
	17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3
DR4Dw4 Purified	+[a]	+	+	+	+	+	+	+	+	+	+	+	+	+	-
Chimeric DR-IE purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-
Lysozyme	-[b]	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Transferrin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BSA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Human gamma globulin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

a. In Elisa, OD (at 370 nm - background): >1.5

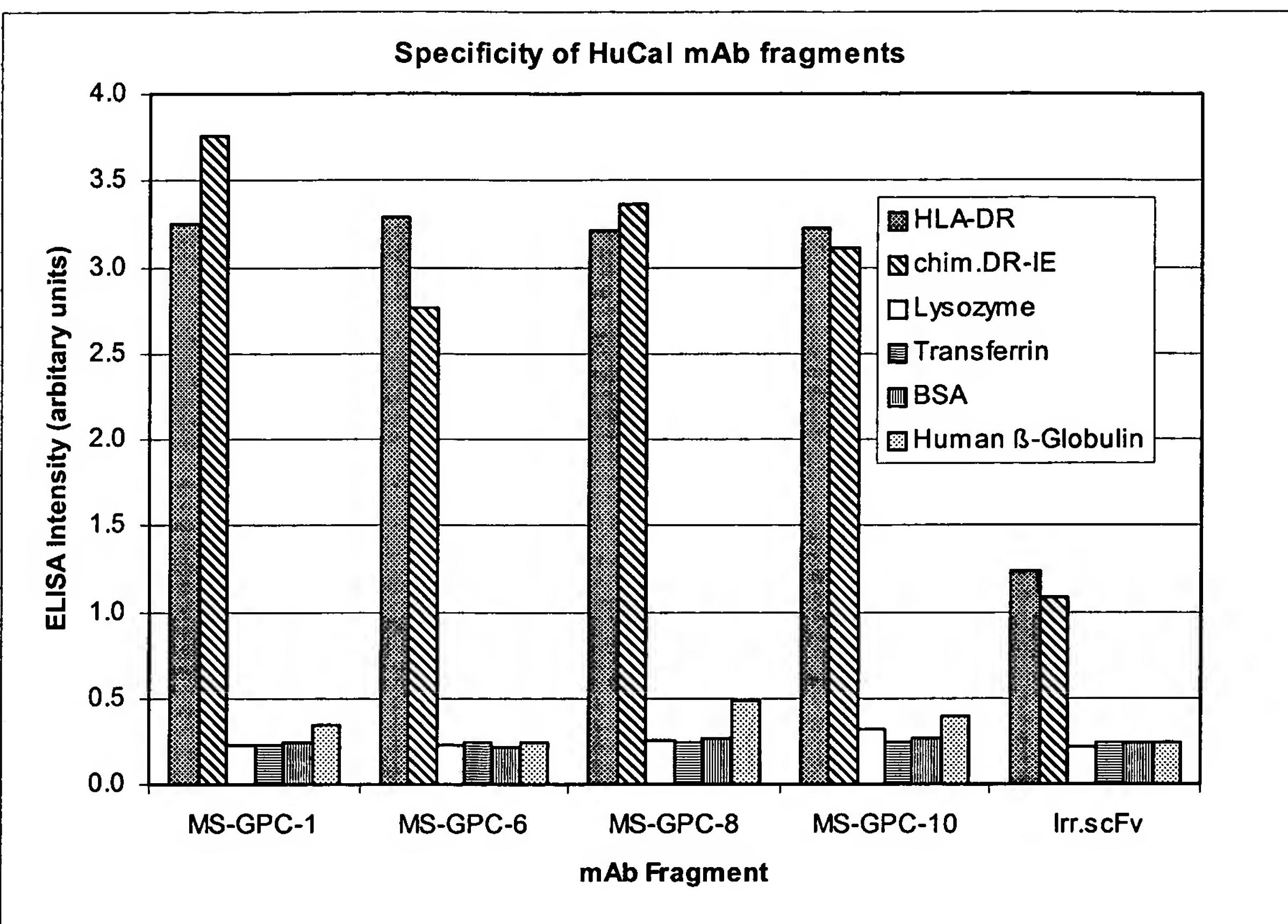b. In Elisa, OD (at 370 nm - background): <0.5

Figure 1b

Specificity of HuCal mAb fragments

Chart legend:
- HLA-DR
- chim.DR-IE
- Lysozyme
- Transferrin
- BSA
- Human ß-Globulin

Y-axis: ELISA Intensity (arbitary units), from 0.0 to 4.0

X-axis: mAb Fragment — MS-GPC-1, MS-GPC-6, MS-GPC-8, MS-GPC-10, Irr.scFv

Figure 2

Cell Line	HLA-	DRB1*	scFv												IgG		
			17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3
LG2	DR1	0101	+[a]	+	[b]	-	+	+	+	+	+	+	+	+	+	+	+
E4181324	DR2	15021	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
VAVY	DR3	0301	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
PRIESS	DR4Dw4	0401	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+/-[c]
TS10	DR4Dw10	0402	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+
BIN40	DR4Dw14	0404	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+
TAB089	DR8	8031	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+
DKB	DR9	9012	+	+	+/-	+/-	+	+	+	+	+	+	+	+	+	+	+/-
WT47	DR13	1302	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
TEM	DR14	1401	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+
L105.1	DRw52	B3*0101	+	-	-	-	nt[d]	+	-	+	+	+	nt	nt	+/-	+/-	+/-
L257.6	DRw53	B4*0101	+/-	-	+	-	nt	+	-	+	+/-	+/-	nt	nt	+	+	+
L25.4	DPw4/w4.2	DP0103/0402	-	-	-	-	nt	+	-	-	-	-	nt	nt	+/-	-	+/-
L256.12	DPw2/w2.1	DP0202/0201	-	-	-	-	nt	+/-	-	-	-	-	nt	nt	-	-	-
L21.3	DQ7/w2	DQ0201/0602	-	-	-	-	nt	+	-	+	-	-	nt	nt	nt	nt	nt
Target Cell																	
PRIESS	% Cells Killed[e]		75	20	28	32	22	89	33	59	75	34	1	5	88	93	74

a. FACS analysis, mAb + FITC-anti human IgG$_4$, mean fluorescence intensity > 30.

b. Mean fluorescence intensity < 10.

c. Mean fluorescence intensity 10-30.

d. Not tested.

e. Based on viable cell recovery after treatment with 200 nM scFv plus 100 nM anti-FLAG or 50 nM mab at 37 C for 4h. Determined by light.
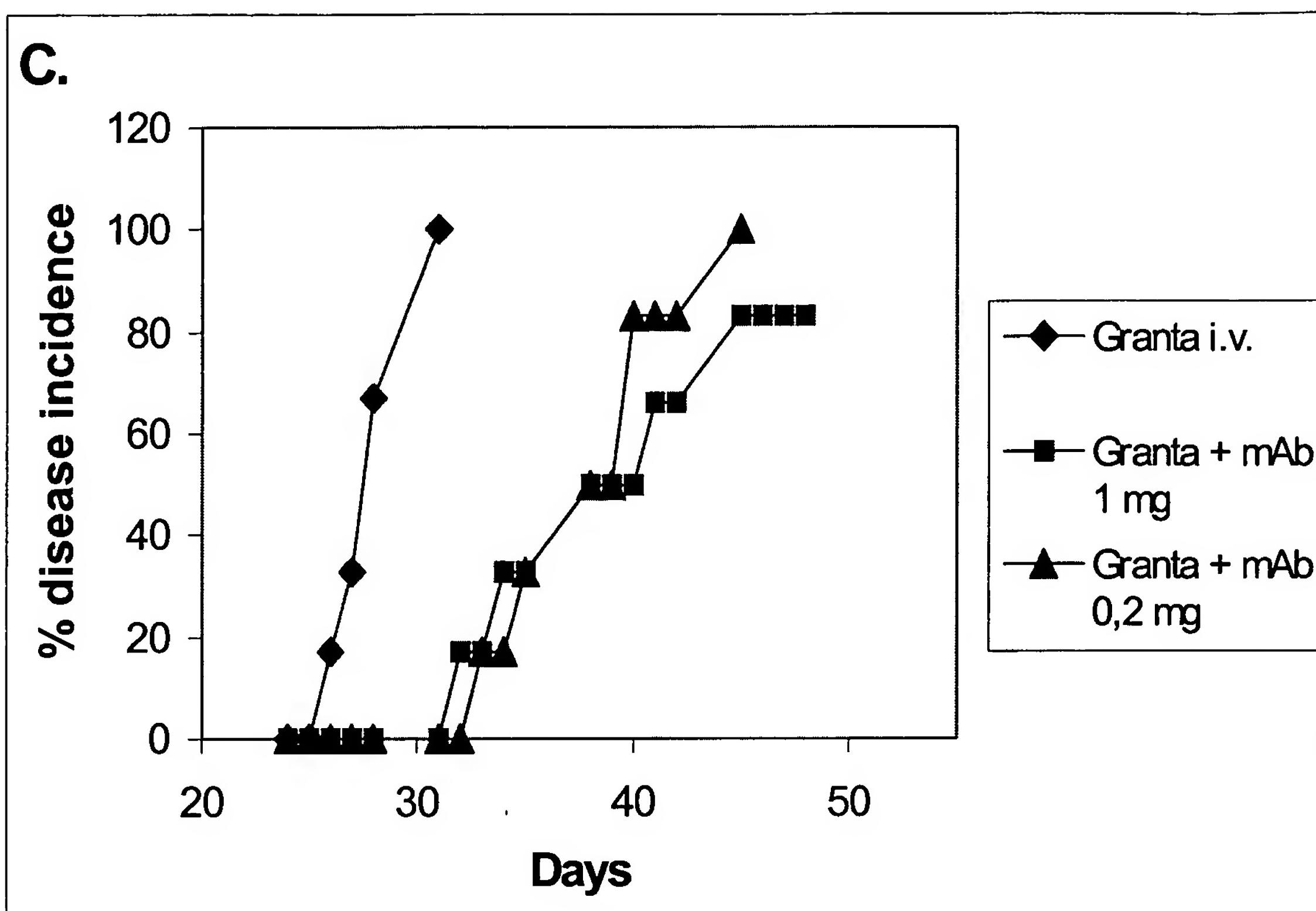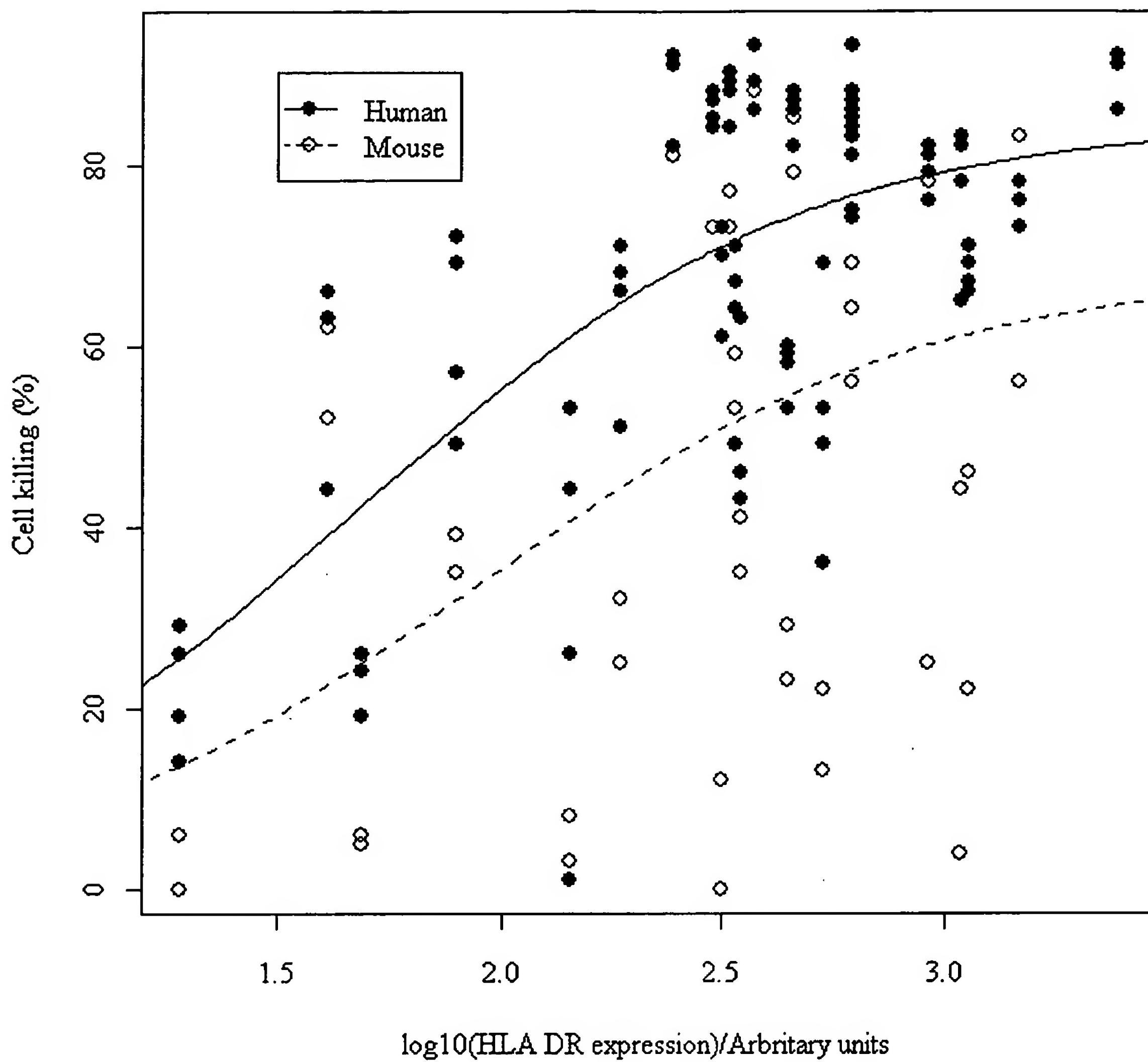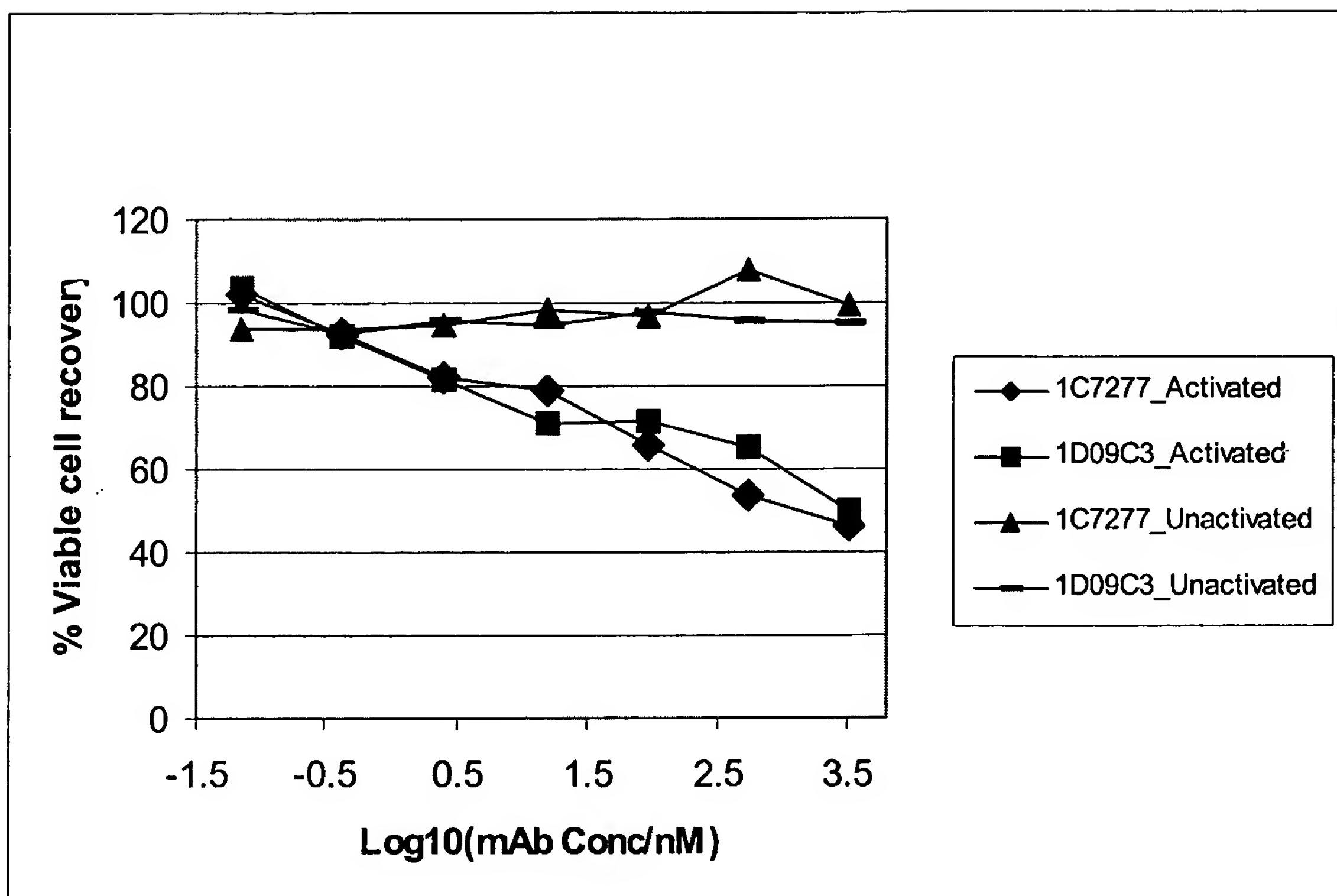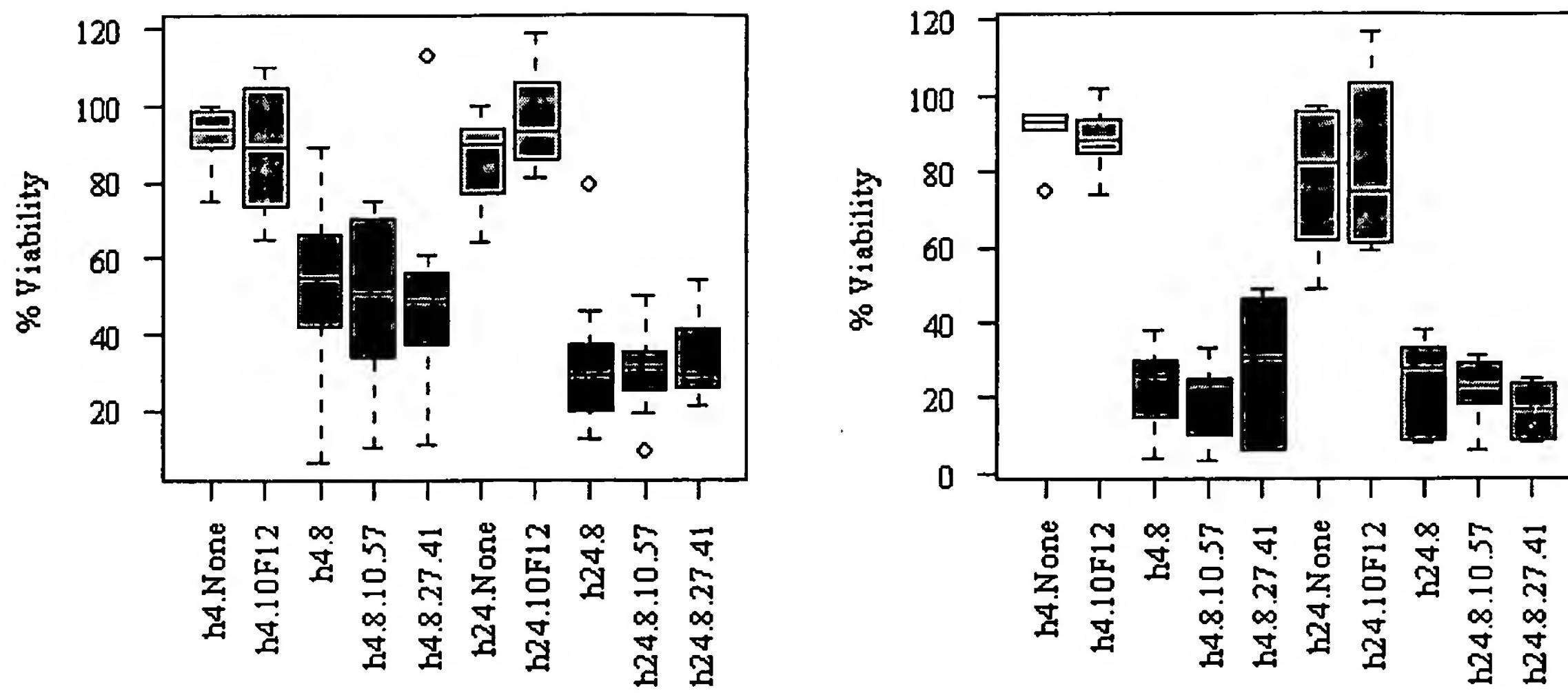
Figure 3

Figure 4

Figure 5

Chart:
- Y-axis: % Viable cell recover)
- X-axis: Log10(mAb Conc/nM)
- Legend:
  - ◆ 1C7277_Activated
  - ■ 1D09C3_Activated
  - ▲ 1C7277_Unactivated
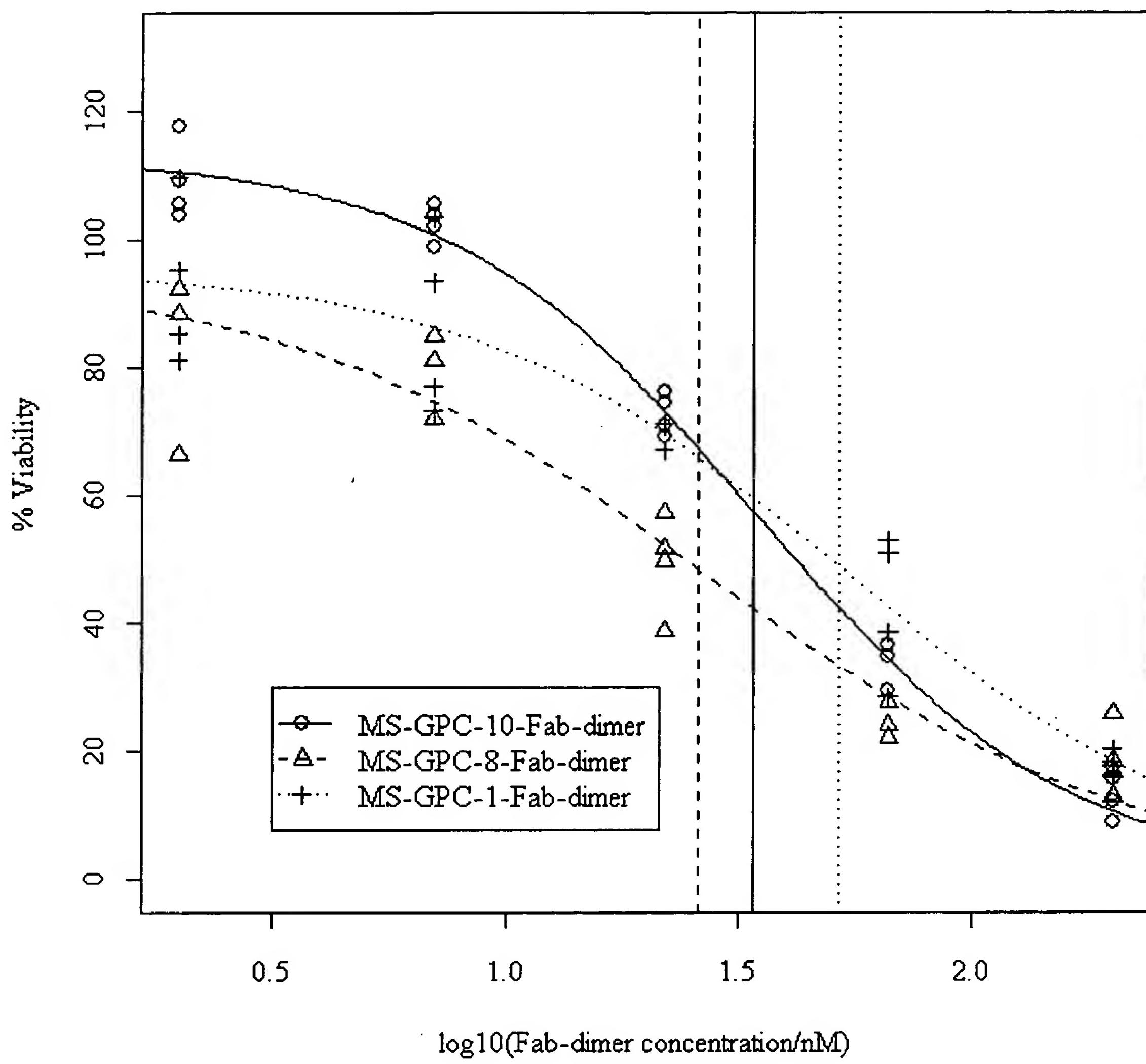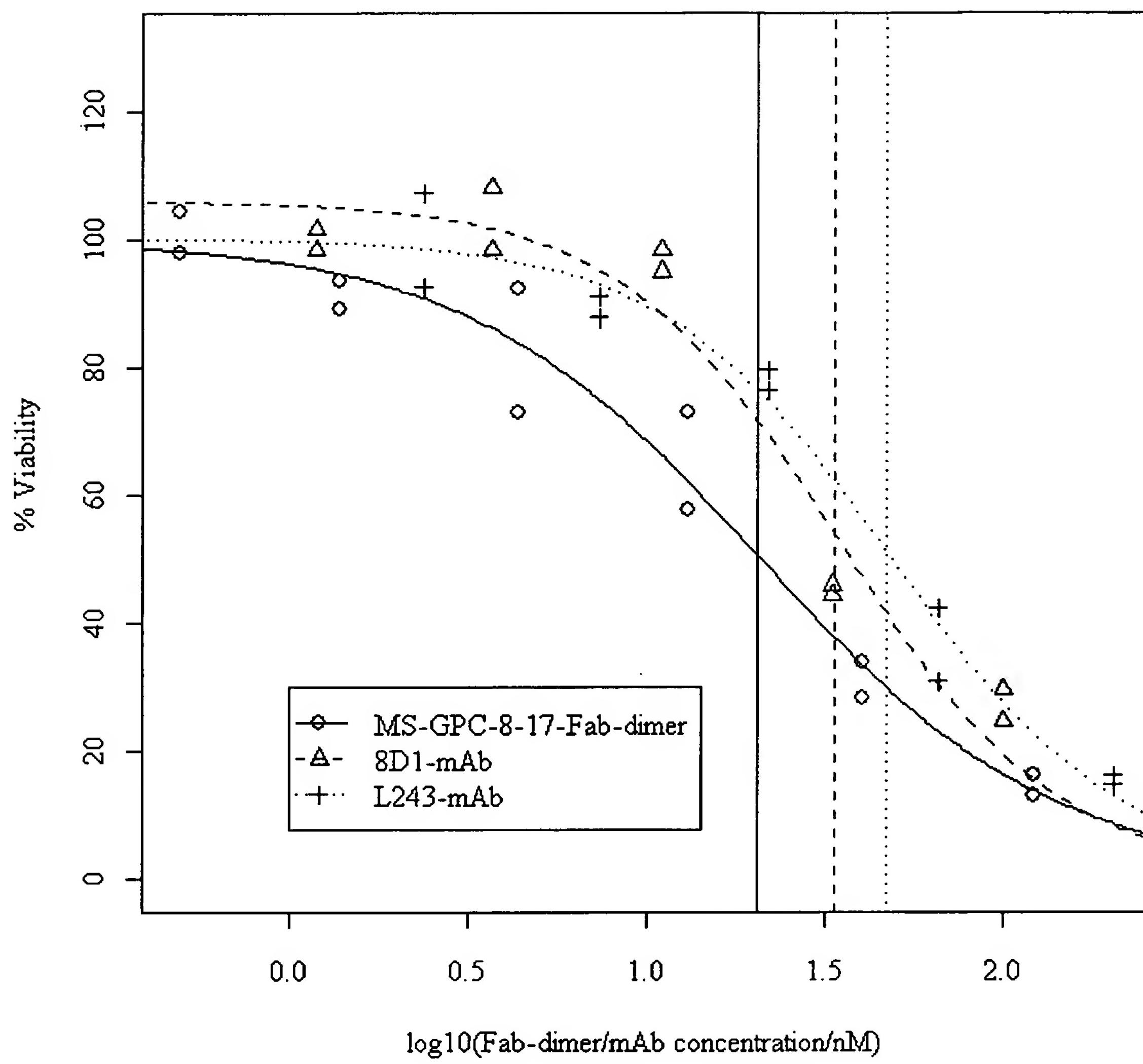 - ▬ 1D09C3_Unactivated
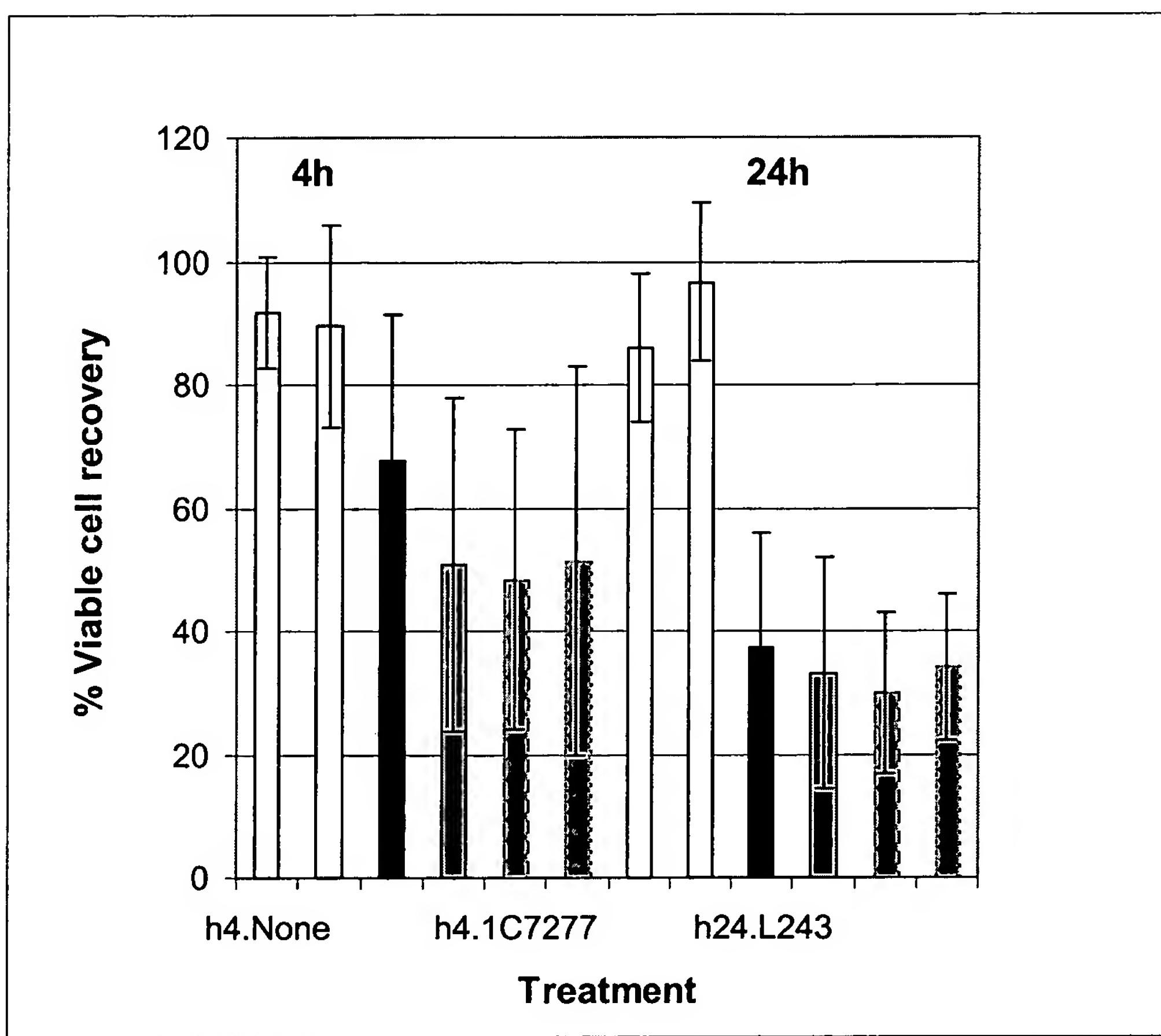
Figure 6a

Figure 6b

Figure 6c
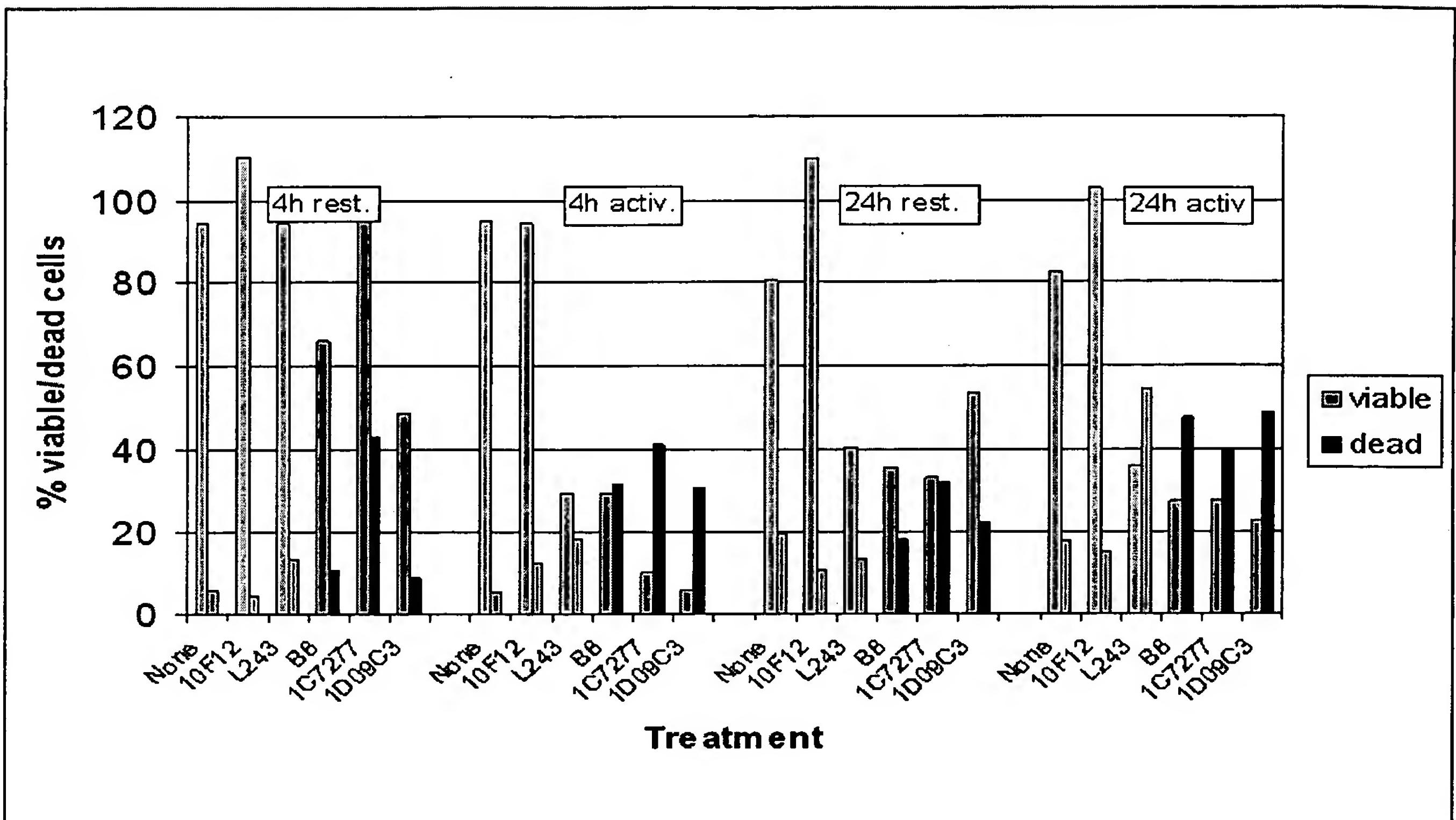
Figure 7a

Figure 7b

Figure 7c
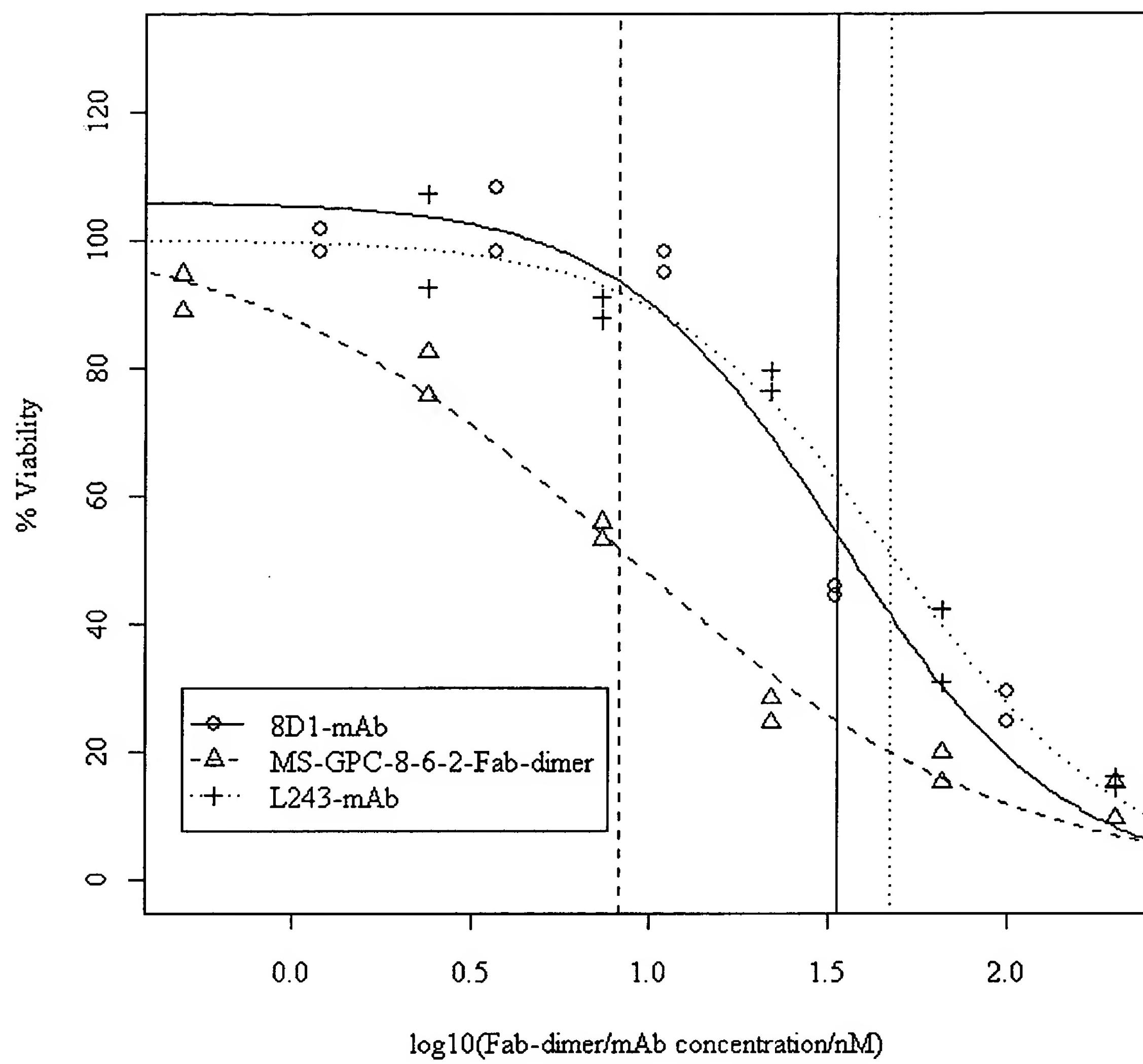
Figure 7d
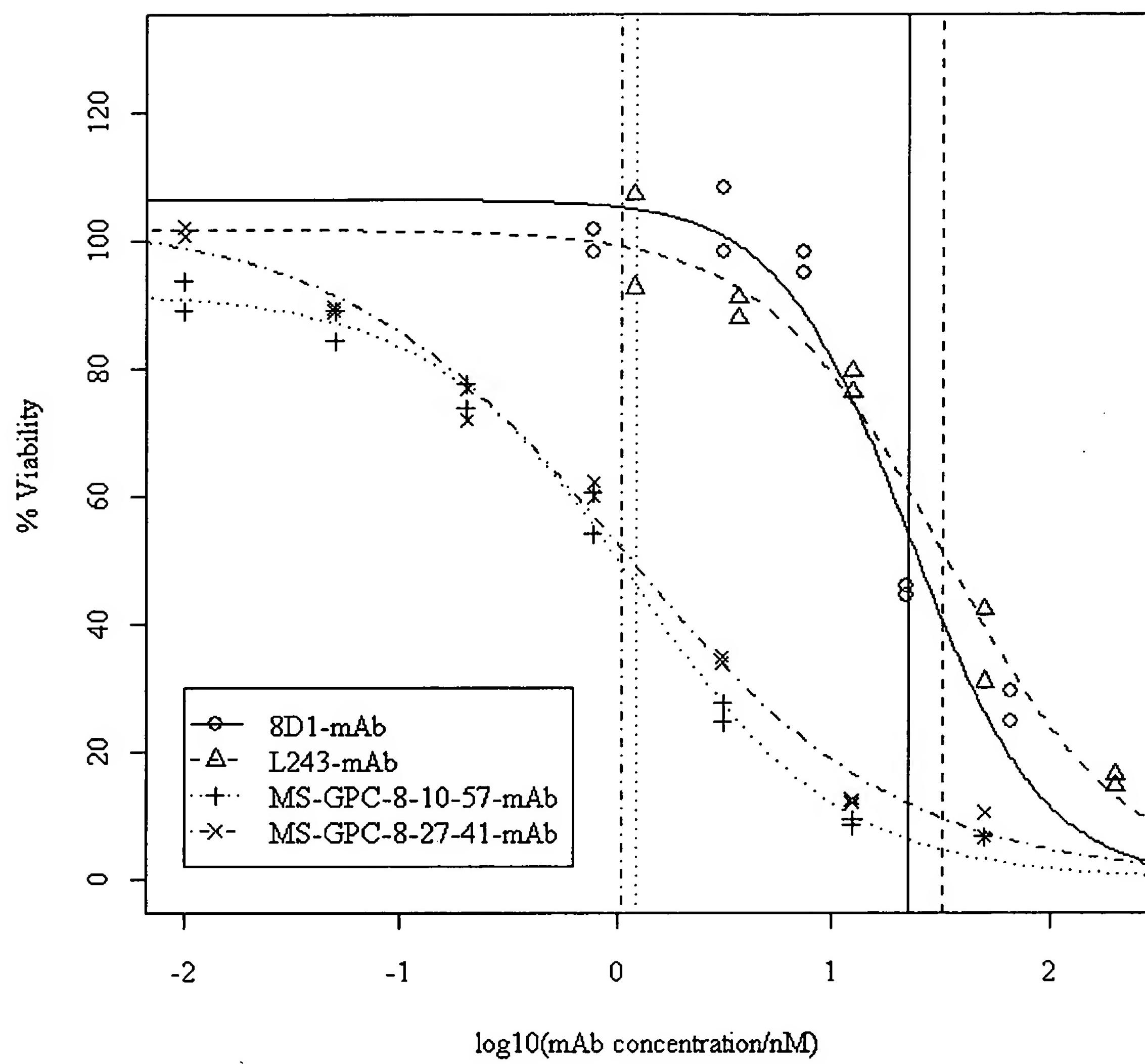
Figure 8a
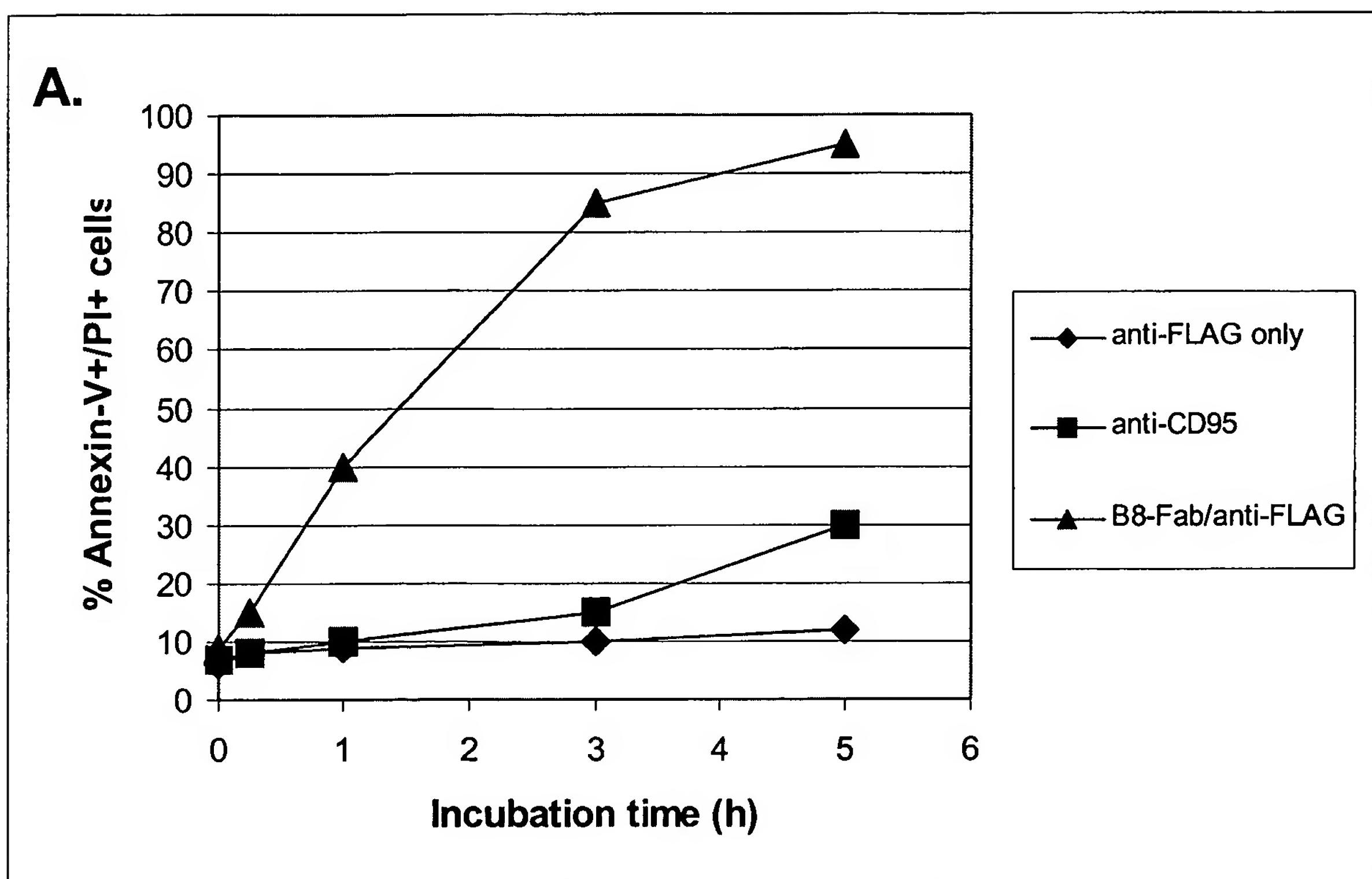
Figure 8b
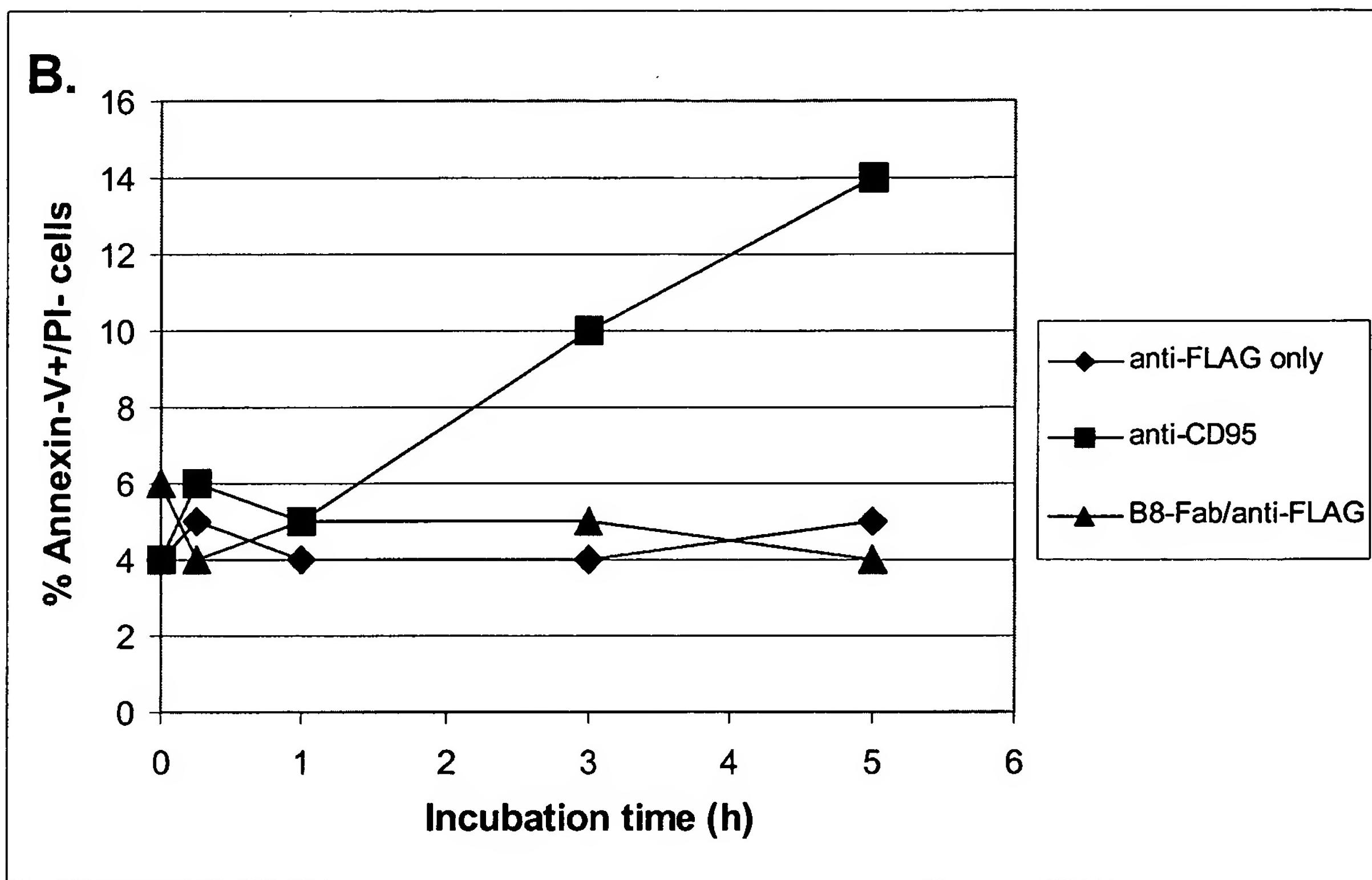
Figure 8c
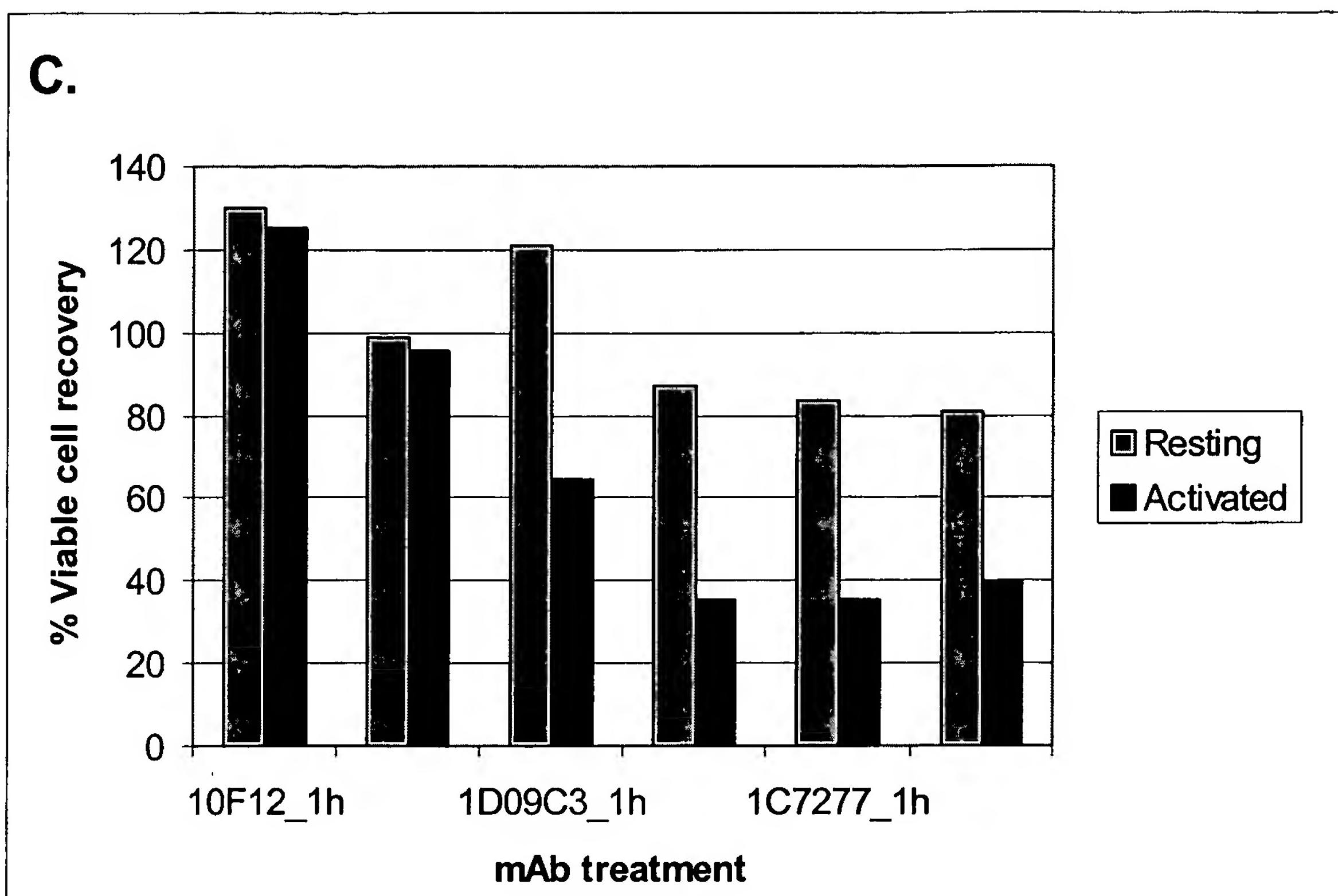
Figure 9a
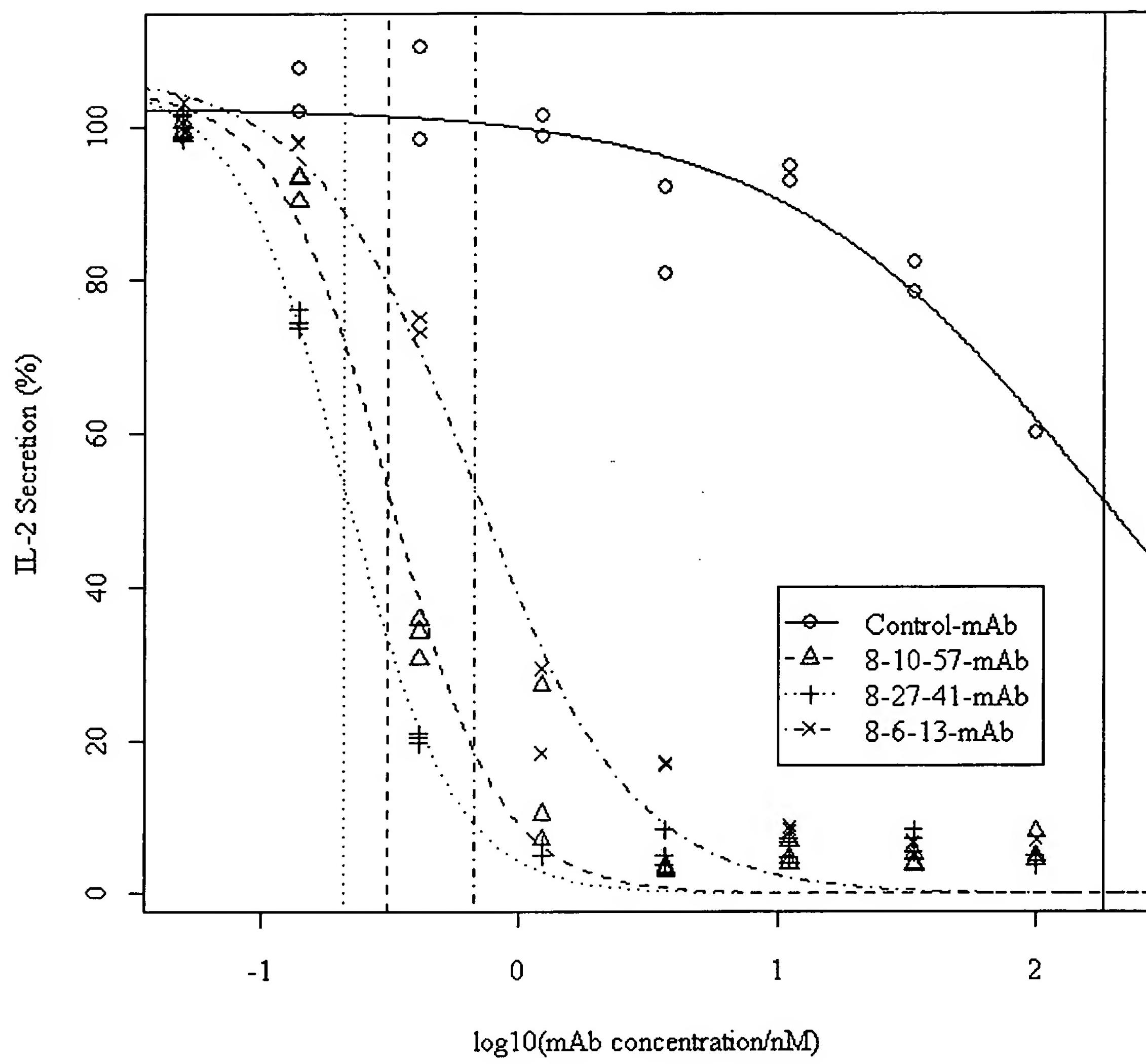
Figure 9b

Figure 9c

Figure 9d

Cell line NG-TcL HA-10

Legend:
- Control HgG4 (●)
- Mouse 1-1C4 (+)
- GPC 2
- GPC 1

X-axis: Mab (nM)
Y-axis: Proliferation (cpm)

Figure 9e

Figure 9f

DR14-tg anti-OVA

Legend:
- GPC 1
- GPC 2
- Mouse L243
- Mouse 11C4

Y-axis: cpm (0, 20000, 40000, 60000, 80000, 100000, 120000)
X-axis: Mab nM (0.1, 1, 10, 100, 1000)
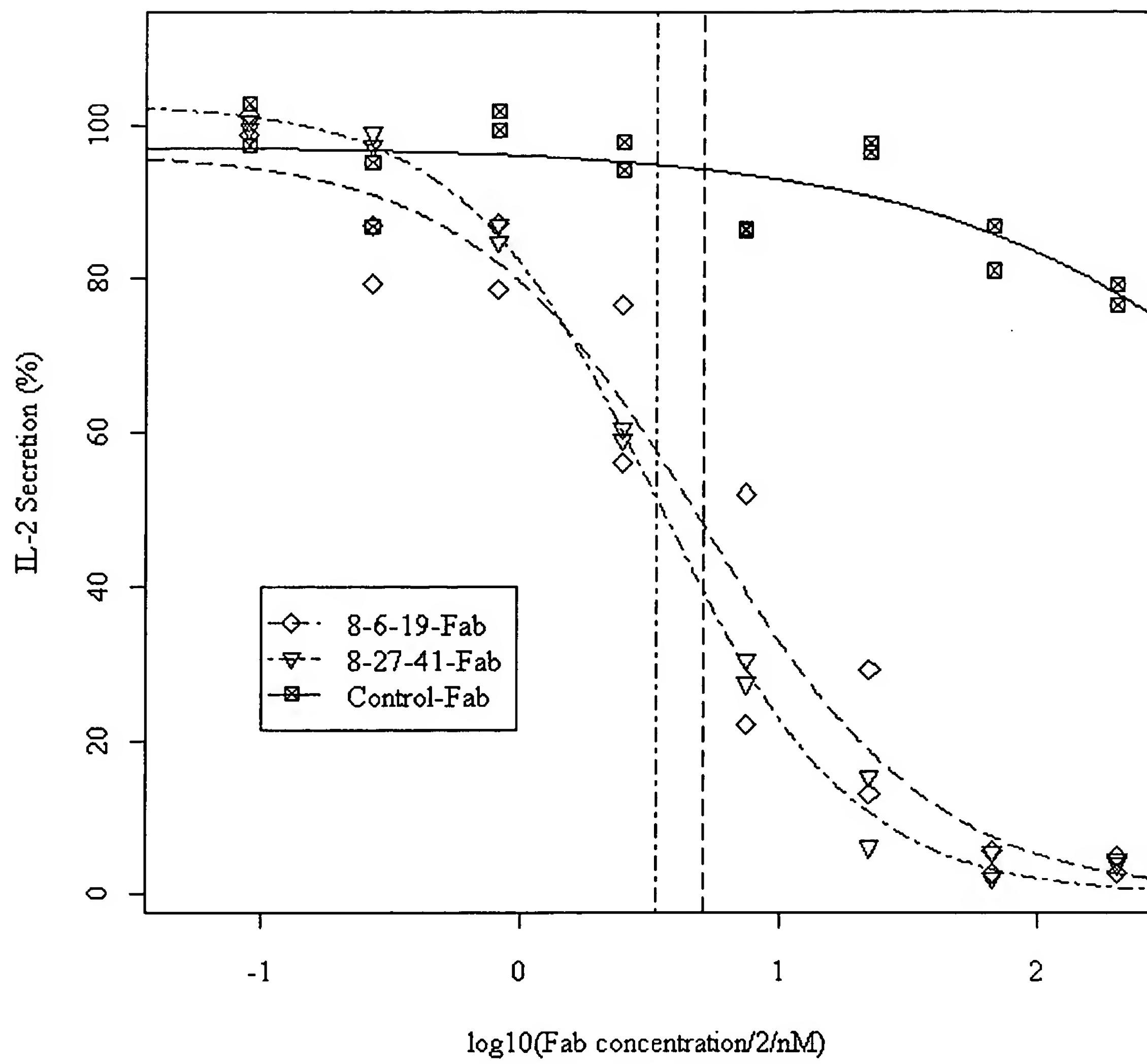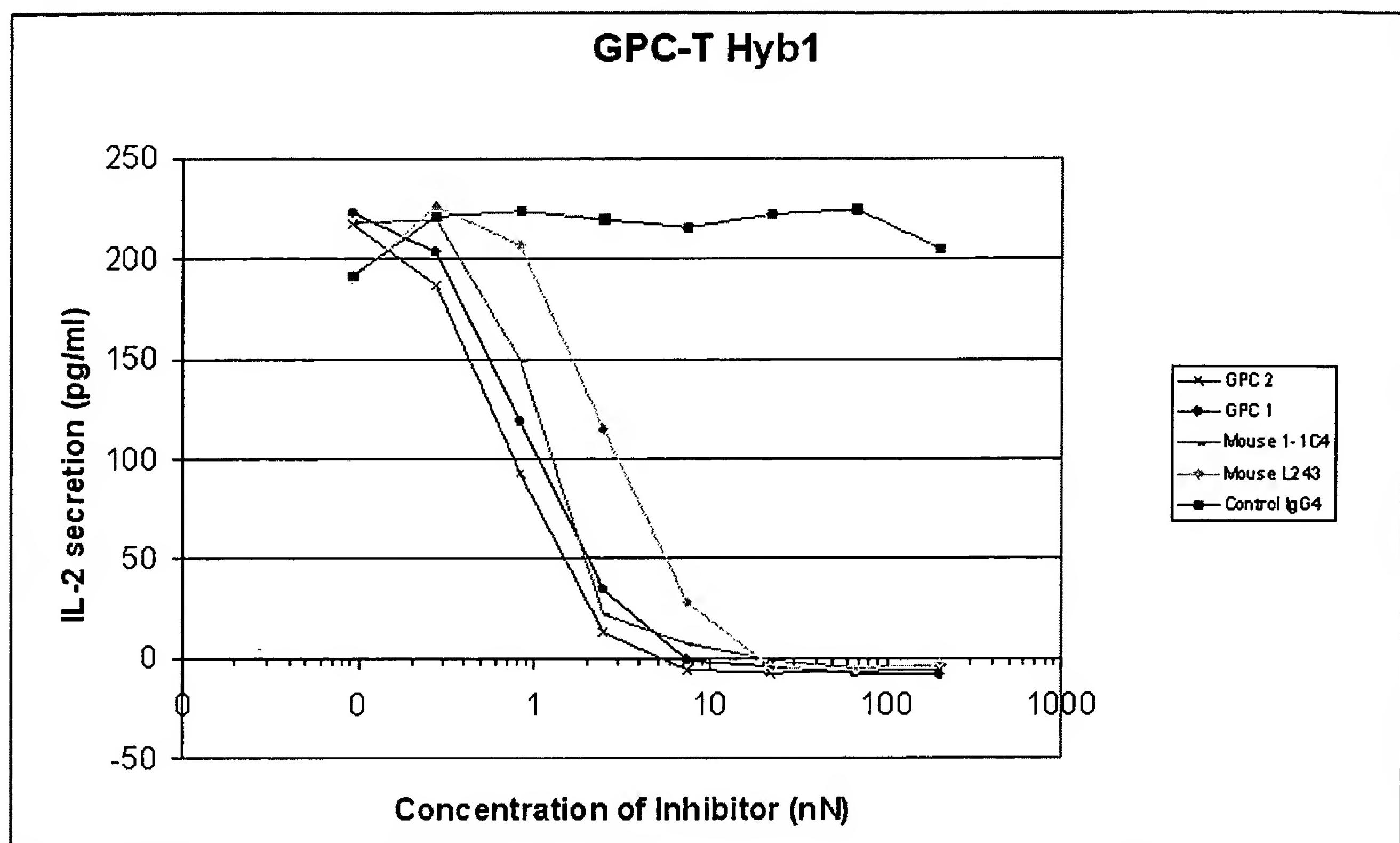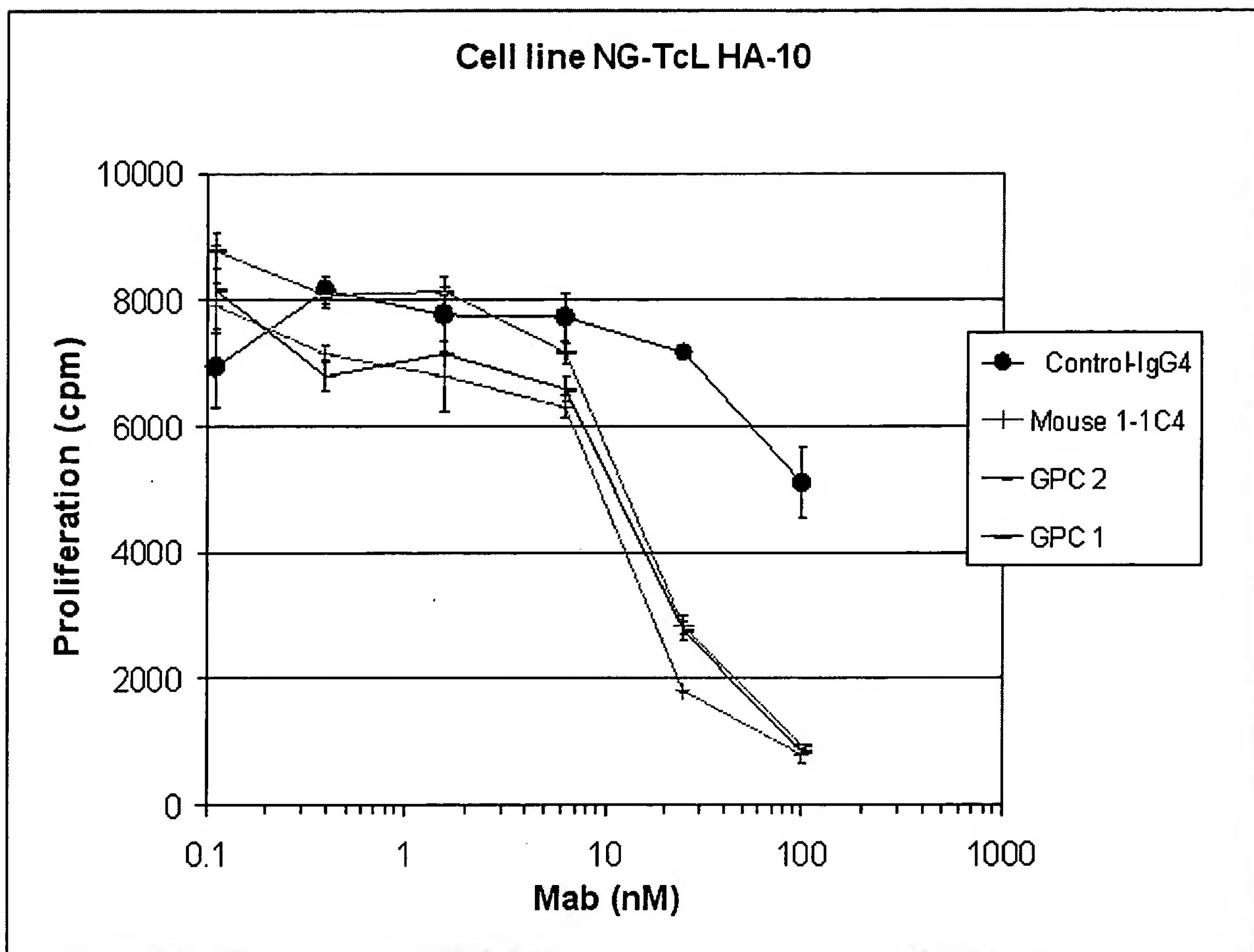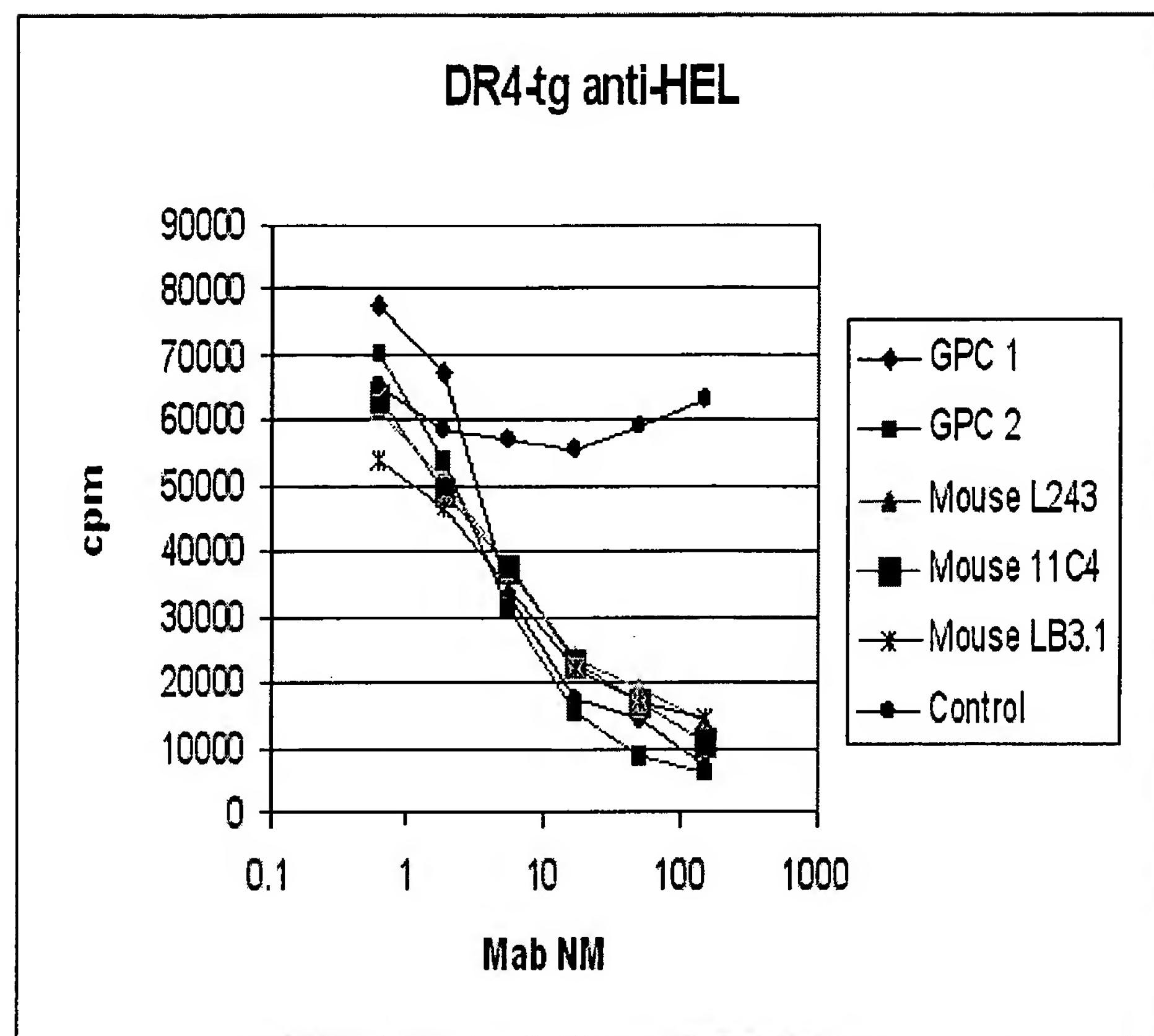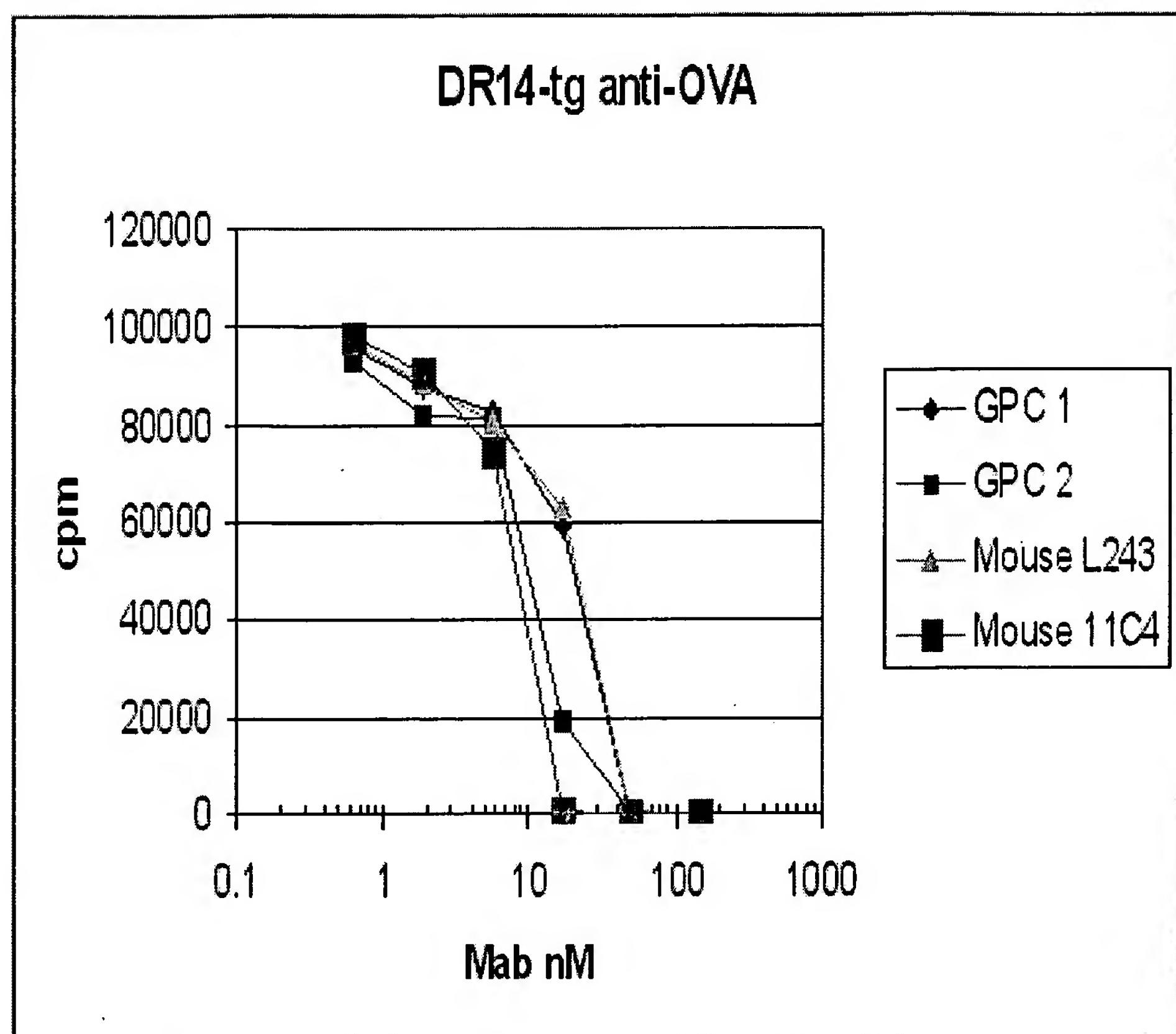
Figure 9g

Figure 9h

DTH to DNFB
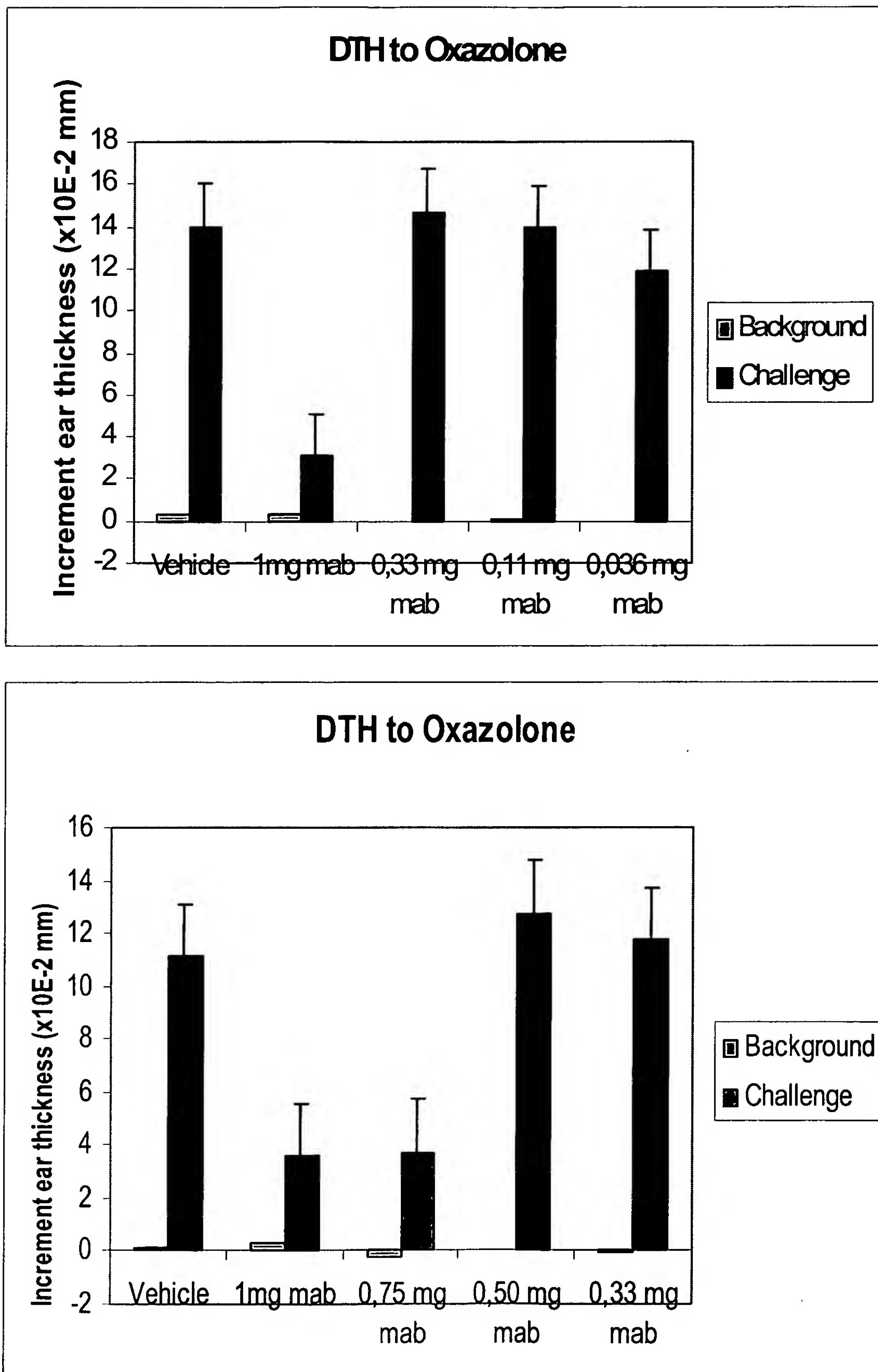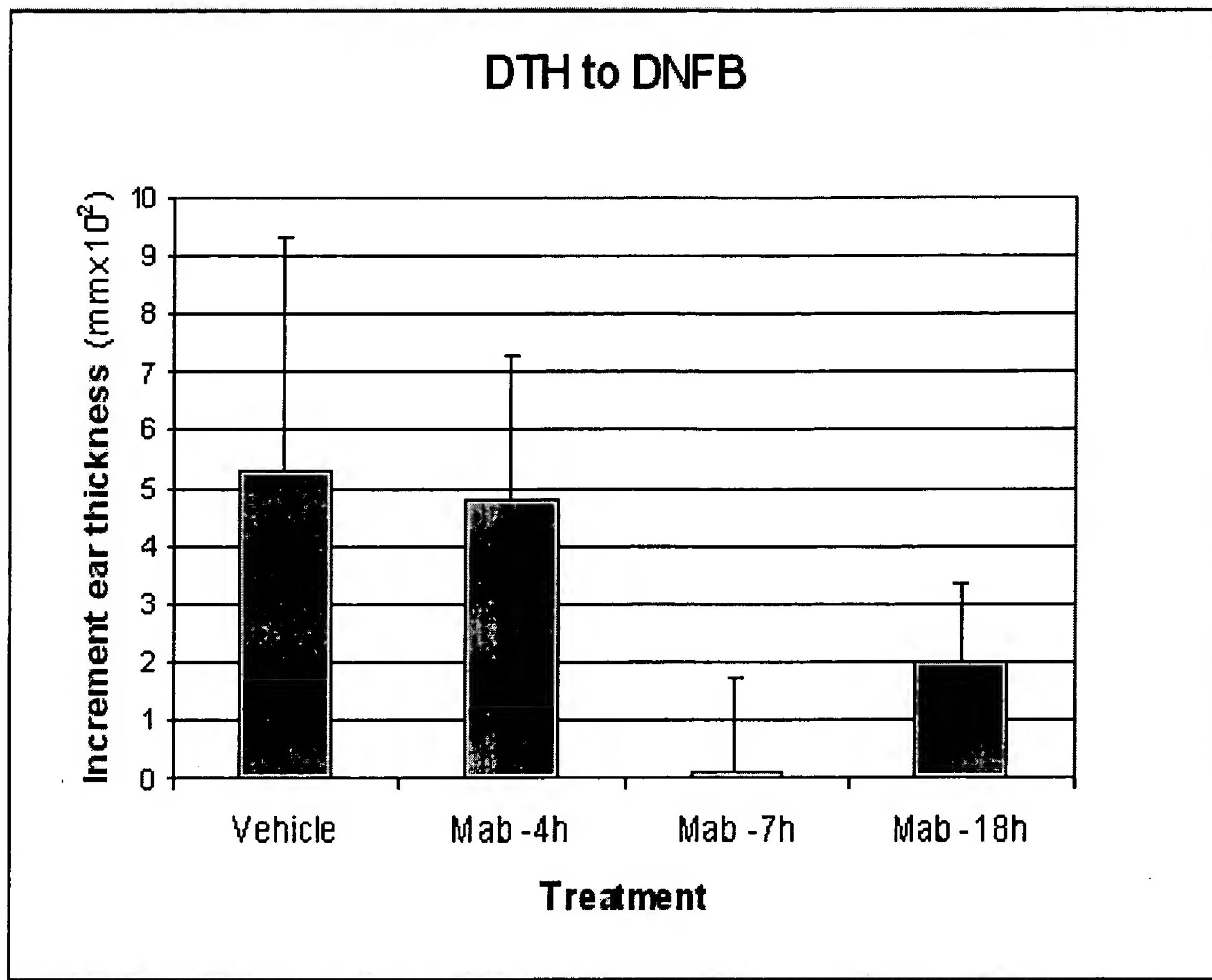
mAb: 1D09C3

Figure 9I

DTH to DNFB
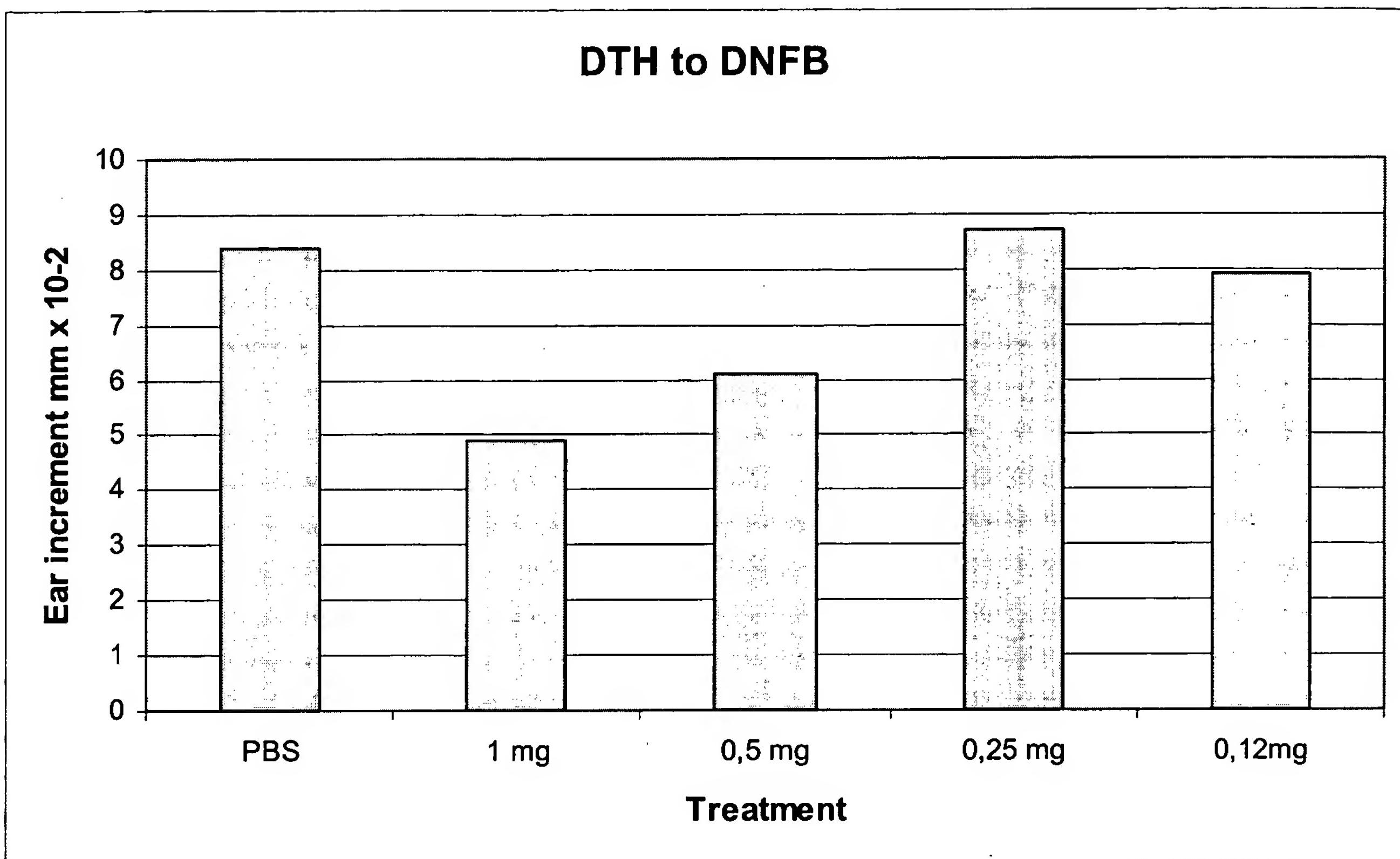
mAb: 1D09C3

Figure 10

Figure 11

pMorph13 scFv
3548 bp
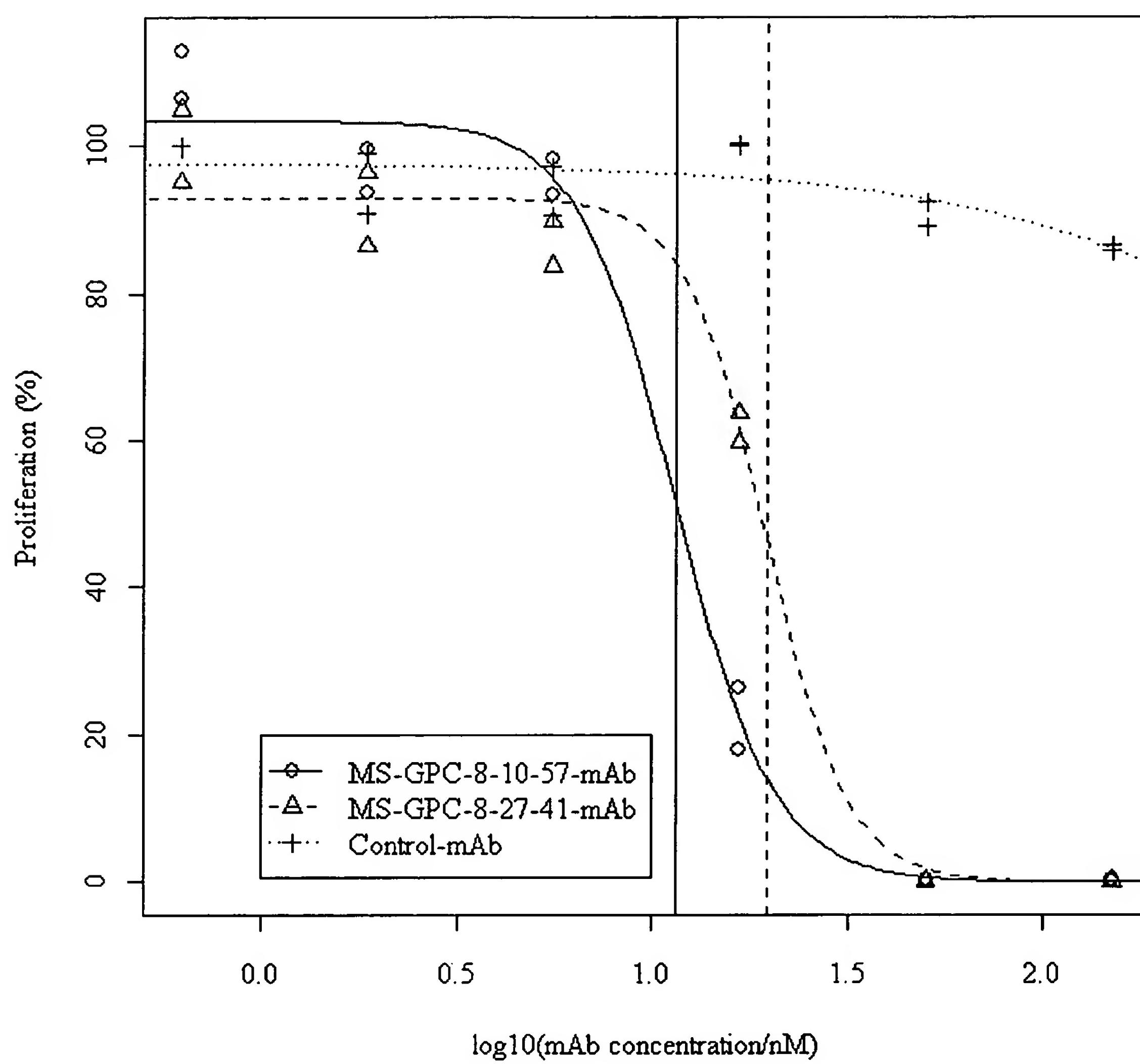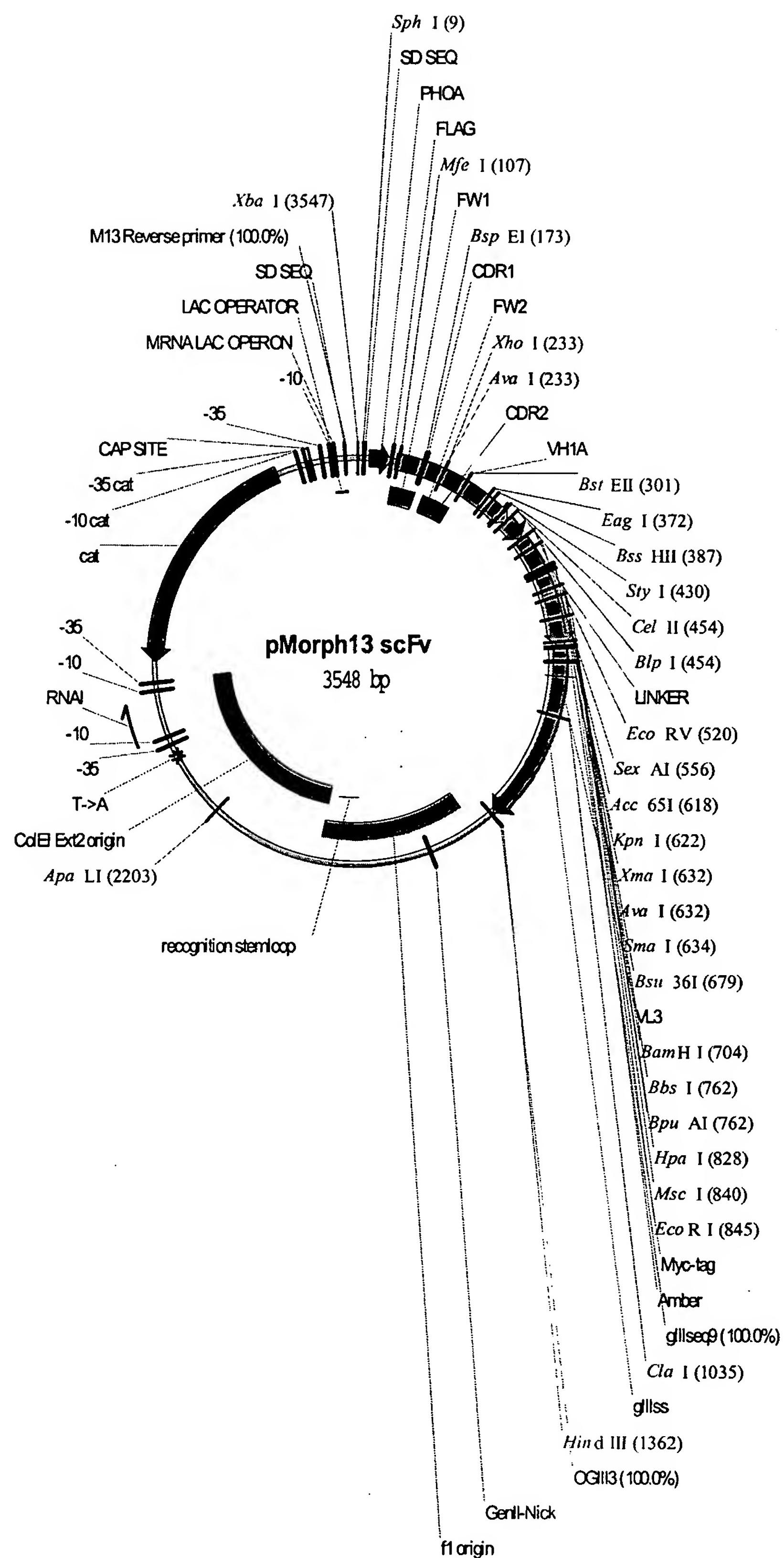
Figure 11 (cont.)

```
    XbaISphI
    ~~~~~~~~~
  1 AGAGCATGCG TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC
    TCTCGTACGC ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG


 51 ACTCTTACCG TTGCTCTTCA CCCCTGTTAC CAAAGCCGAC TACAAAGATG
    TGAGAATGGC AACGAGAAGT GGGGACAATG GTTTCGGCTG ATGTTTCTAC


         MfeI
         ~~~~~~~
101 AAGTGCAATT GGTTCAGTCT GGCGCGGAAG TGAAAAAACC GGGCAGCAGC
    TTCACGTTAA CCAAGTCAGA CCGCGCCTTC ACTTTTTTGG CCCGTCGTCG


                        BspEI
                        ~~~~~~
151 GTGAAAGTGA GCTGCAAAGC CTCCGGAGGC ACTTTTAGCA GCTATGCGAT
    CACTTTCACT CGACGTTTCG GAGGCCTCCG TGAAAATCGT CGATACGCTA


                             XhoI
                             ~~~~~~
                             AvaI
                             ~~~~~~
201 TAGCTGGGTG CGCCAAGCCC CTGGGCAGGG TCTCGAGTGG ATGGGCGGCA
    ATCGACCCAC GCGGTTCGGG GACCCGTCCC AGAGCTCACC TACCCGCCGT


                                            BstEII
                                            ~
251 TTATTCCGAT TTTTGGCACG GCGAACTACG CGCAGAAGTT TCAGGGCCGG
    AATAAGGCTA AAAACCGTGC CGCTTGATGC GCGTCTTCAA AGTCCCGGCC


    BstEII
    ~~~~~~
301 GTGACCATTA CCGCGGATGA AAGCACCAGC ACCGCGTATA TGGAACTGAG
    CACTGGTAAT GGCGCCTACT TTCGTGGTCG TGGCGCATAT ACCTTGACTC


                        EagI            BssHII
                        ~~~~~~          ~~~~~~~
351 CAGCCTGCGT AGCGAAGATA CGGCCGTGTA TTATTGCGCG CGTTATTATG
    GTCGGACGCA TCGCTTCTAT GCCGGCACAT AATAACGCGC GCAATAATAC


                             StyI
                             ~~~~~~~
401 ATCGTATGTA TAATATGGAT TATTGGGGCC AAGGCACCCT GGTGACGGTT
    TAGCATACAT ATTATACCTA ATAACCCCGG TTCCGTGGGA CCACTGCCAA


       BlpI
       ~~~~~~~
       CelII
       ~~~~~~~
451 AGCTCAGCGG GTGGCGGTTC TGGCGGCGGT GGGAGCGGTG GCGGTGGTTC
    TCGAGTCGCC CACCGCCAAG ACCGCCGCCA CCCTCGCCAC CGCCACCAAG


              EcoRV
              ~~~~~~~
501 TGGCGGTGGT GGTTCCGATA TCGAACTGAC CCAGCCGCCT TCAGTGAGCG
```

ACCGCCACCA CCAAGGCTAT AGCTTGACTG GGTCGGCGGA AGTCACTCGC

SexAI
~~~~~~~
551 TTGCACCAGG TCAGACCGCG CGTATCTCGT GTAGCGGCGA TGCGCTGGGC
     AACGTGGTCC AGTCTGGCGC GCATAGAGCA CATCGCCGCT ACGCGACCCG

                                        XmaI
                                        ~~~~~~
                        KpnI   SmaI
                        ~~~~~~~   ~~~~~~
                        Acc65I   AvaI
                        ~~~~~~~   ~~~~~~
601 GATAAATACG CGAGCTGGTA CCAGCAGAAA CCCGGGCAGG CGCCAGTTCT
     CTATTTATGC GCTCGACCAT GGTCGTCTTT GGGCCCGTCC GCGGTCAAGA

                                    Bsu36I
                                    ~~~~~~~~
651 GGTGATTTAT GATGATTCTG ACCGTCCCTC AGGCATCCCG GAACGCTTTA
     CCACTAAATA CTACTAAGAC TGGCAGGGAG TCCGTAGGGC CTTGCGAAAT

                BamHI
                ~~~~~~
701 GCGGATCCAA CAGCGGCAAC ACCGCGACCC TGACCATTAG CGGCACTCAG
     CGCCTAGGTT GTCGCCGTTG TGGCGCTGGG ACTGGTAATC GCCGTGAGTC

                BpuAI
                ~~~~~~
                BbsI
                ~~~~~~
751 GCGGAAGACG AAGCGGATTA TTATTGCCAG AGCTATGACG CTCATATGCG
     CGCCTTCTGC TTCGCCTAAT AATAACGGTC TCGATACTGC GAGTATACGC

                                HpaI   MscI   EcoRI
                                ~~~~~~   ~~~~~~~   ~~~~~~
801 TCCTGTGTTT GGCGGCGGCA CGAAGTTAAC CGTTCTTGGC CAGGAATTCG
     AGGACACAAA CCGCCGCCGT GCTTCAATTG GCAAGAACCG GTCCTTAAGC

851 AGCAGAAGCT GATCTCTGAG GAGGATCTGA ACTAGGGTGG TGGCTCTGGT
     TCGTCTTCGA CTAGAGACTC CTCCTAGACT TGATCCCACC ACCGAGACCA

901 TCCGGTGATT TTGATTATGA AAAGATGGCA AACGCTAATA AGGGGGCTAT
     AGGCCACTAA AACTAATACT TTTCTACCGT TTGCGATTAT TCCCCCGATA
                                     gIIIseq9 100.0%
                                ====================

951 GACCGAAAAT GCCGATGAAA ACGCGCTACA GTCTGACGCT AAAGGCAAAC
     CTGGCTTTTA CGGCTACTTT TGCGCGATGT CAGACTGCGA TTTCCGTTTG

                                        ClaI
                                        ~~~~~~
1001 TTGATTCTGT CGCTACTGAT TACGGTGCTG CTATCGATGG TTTCATTGGT
     AACTAAGACA GCGATGACTA ATGCCACGAC GATAGCTACC AAAGTAACCA

1051 GACGTTTCCG GCCTTGCTAA TGGTAATGGT GCTACTGGTG ATTTTGCTGG
     CTGCAAAGGC CGGAACGATT ACCATTACCA CGATGACCAC TAAAACGACC

```
1101   CTCTAATTCC CAAATGGCTC AAGTCGGTGA CGGTGATAAT TCACCTTTAA
       GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGAAATT

1151   TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTTGAATGT
       ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1201   CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG
       GCGGGAAAAC AGAAACCGCG ACCATTTGGT ATACTTAAAA GATAACTAAC

1251   TGACAAAATA AACTTATTCC GTGGTGTCTT TGCGTTTCTT TTATATGTTG
       ACTGTTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1301   CCACCTTTAT GTATGTATTT CTACGTTTG CTAACATACT GCGTAATAAG
       GGTGGAAATA CATACATAAA GATGCAAAC GATTGTATGA CGCATTATTC


                   HindIII
                   ~~~~~~
1351   GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
       CTCAGAACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                       OGIII3   100.0%
                   ==================
1401   ACATTTTTTT TGTCTGCCGT TTAATGAAAT TGTAAACGTT AATATTTTGT
       TGTAAAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

1451   TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG
       ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

1501   GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
       CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

1551   GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
       CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC

1601   ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
       TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

1651   CGAGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT GCCGTAAAGC
       GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG

1701   ACTAAATCGG AACCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
       TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCCTT

1751   AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC
       TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCG

1801   GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC
       CGATCCCGCG ACCGTTCACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

1851   CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA
       GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT ACACTCGTTT

1901   AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT
       TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

1951   TCCATAGGCT CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT
       AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA
```

2001   CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC
          GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2051   TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT
          ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2101   ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA
          TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2151   CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG
          GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC

           ApaLI
           ~~~~~~
2201   TGTGCACGAA CCCCCCGTTC AGTCCGACCG CTGCGCCTTA TCCGGTAACT
          ACACGTGCTT GGGGGGCAAG TCAGGCTGGC GACGCGGAAT AGGCCATTGA

2251   ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA
          TAGCAGAACT CAGGTTGGGC CATTCTGTGC TGAATAGCGG TGACCGTCGT

2301   GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA
          CGGTGACCAT TGTCCTAATC GTCTCGCTCC ATACATCCGC CACGATGTCT

2351   GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGA ACAGTATTTG
          CAAGAACTTC ACCACCGGAT TGATGCCGAT GTGATCTTCT TGTCATAAAC

2401   GTATCTGCGC TCTGCTGTAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC
          CATAGACGCG AGACGACATC GGTCAATGGA AGCCTTTTTC TCAACCATCG

2451   TCTTGATCCG GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTTGTTTG
          AGAACTAGGC CGTTTGTTTG GTGGCGACCA TCGCCACCAA AAAAACAAAC

2501   CAAGCAGCAG ATTACGCGCA GAAAAAAAGG ATCTCAAGAA GATCCTTTGA
          GTTCGTCGTC TAATGCGCGT CTTTTTTTCC TAGAGTTCTT CTAGGAAACT

2551   TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG
          AGAAAAGATG CCCCAGACTG CGAGTCACCT TGCTTTTGAG TGCAATTCCC

2601   ATTTTGGTCA GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT
          TAAAACCAGT CTAGATCGTG GTCCGCAAAT TCCCGTGGTT ATTGACGGAA

2651   AAAAAAATTA CGCCCCGCCC TGCCACTCAT CGCAGTACTG TTGTAATTCA
          TTTTTTTAAT GCGGGGCGGG ACGGTGAGTA GCGTCATGAC AACATTAAGT

2701   TTAAGCATTC TGCCGACATG GAAGCCATCA CAAACGGCAT GATGAACCTG
          AATTCGTAAG ACGGCTGTAC CTTCGGTAGT GTTTGCCGTA CTACTTGGAC

2751   AATCGCCAGC GGCATCAGCA CCTTGTCGCC TTGCGTATAA TATTTGCCCA
          TTAGCGGTCG CCGTAGTCGT GGAACAGCGG AACGCATATT ATAAACGGGT

2801   TAGTGAAAAC GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA
          ATCACTTTTG CCCCCGCTTC TTCAACAGGT ATAACCGATG CAAATTTAGT

2851   AAACTGGTGA AACTCACCCA GGGATTGGCT GAGACGAAAA ACATATTCTC
          TTTGACCACT TTGAGTGGGT CCCTAACCGA CTCTGCTTTT TGTATAAGAG

```
2901   AATAAACCCT  TTAGGGAAAT  AGGCCAGGTT  TTCACCGTAA  CACGCCACAT
       TTATTTGGGA  AATCCCTTTA  TCCGGTCCAA  AAGTGGCATT  GTGCGGTGTA

2951   CTTGCGAATA  TATGTGTAGA  AACTGCCGGA  AATCGTCGTG  GTATTCACTC
       GAACGCTTAT  ATACACATCT  TTGACGGCCT  TTAGCAGCAC  CATAAGTGAG

3001   CAGAGCGATG  AAAACGTTTC  AGTTTGCTCA  TGGAAAACGG  TGTAACAAGG
       GTCTCGCTAC  TTTTGCAAAG  TCAAACGAGT  ACCTTTTGCC  ACATTGTTCC

3051   GTGAACACTA  TCCCATATCA  CCAGCTCACC  GTCTTTCATT  GCCATACGGA
       CACTTGTGAT  AGGGTATAGT  GGTCGAGTGG  CAGAAAGTAA  CGGTATGCCT

3101   ACTCCGGGTG  AGCATTCATC  AGGCGGGCAA  GAATGTGAAT  AAAGGCCGGA
       TGAGGCCCAC  TCGTAAGTAG  TCCGCCCGTT  CTTACACTTA  TTTCCGGCCT

3151   TAAAACTTGT  GCTTATTTTT  CTTTACGGTC  TTTAAAAAGG  CCGTAATATC
       ATTTTGAACA  CGAATAAAAA  GAAATGCCAG  AAATTTTTCC  GGCATTATAG

3201   CAGCTGAACG  GTCTGGTTAT  AGGTACATTG  AGCAACTGAC  TGAAATGCCT
       GTCGACTTGC  CAGACCAATA  TCCATGTAAC  TCGTTGACTG  ACTTTACGGA

3251   CAAAATGTTC  TTTACGATGC  CATTGGGATA  TATCAACGGT  GGTATATCCA
       GTTTTACAAG  AAATGCTACG  GTAACCCTAT  ATAGTTGCCA  CCATATAGGT

3301   GTGATTTTTT  TCTCCATTTT  AGCTTCCTTA  GCTCCTGAAA  ATCTCGATAA
       CACTAAAAAA  AGAGGTAAAA  TCGAAGGAAT  CGAGGACTTT  TAGAGCTATT

3351   CTCAAAAAAT  ACGCCCGGTA  GTGATCTTAT  TTCATTATGG  TGAAAGTTGG
       GAGTTTTTTA  TGCGGGCCAT  CACTAGAATA  AAGTAATACC  ACTTTCAACC

3401   AACCTCACCC  GACGTCTAAT  GTGAGTTAGC  TCACTCATTA  GGCACCCCAG
       TTGGAGTGGG  CTGCAGATTA  CACTCAATCG  AGTGAGTAAT  CCGTGGGGTC

3451   GCTTTACACT  TTATGCTTCC  GGCTCGTATG  TTGTGTGGAA  TTGTGAGCGG
       CGAAATGTGA  AATACGAAGG  CCGAGCATAC  AACACACCTT  AACACTCGCC

                      M13 Reverse  primer 100.0%              XbaI
                      ===================                     ~~
3501   ATAACAATTT  CACACAGGAA  ACAGCTATGA  CCATGATTAC  GAATTTCT
       TATTGTTAAA  GTGTGTCCTT  TGTCGATACT  GGTACTAATG  CTTAAAGA
```

Figure 12

Xba I (2)
Sph I (12)
SD SEQ
PHOA
FLAG
Mfe I (110)
FW1
Bsp EI (176)
CDR1
FW2
Ava I (236)
Xho I (236)
CDR2
VH3
Nsp V (326)
Sfu I (326)
Bst BI (326)
FW3
Eag I (375)
Bss HII (390)
CDR3
Sty I (442)
Cel II (466)
Blp I (466)
scFv
LINKER
Eco RV (532)
FW1
Pst I (599)
CDR1
Acc 651 (648)
Kpn I (652)
Bex AI (661)
FW2
CDR2
Vk2
BamH I (740)
FW3
Bbs I (792)
Bpu AI (792)
CDR3
FW4
Msc I (840)
Bsi WI (866)
Eco R I (872)
Flagtag
Bss HII (903)
StreptagII
Hind III (939)
OGIII3 (100.0%)
functional ssori
GenII-Nick
T-->G
G-->C
recognition stemloop
Insert GGCCTTTTGCT

M13 Reverse primer (100.0%)
SD SEQ
lac p/o
MRNA LAC OPERON
LAC OPERATOR
-10
-35
deletion of T
CAP SITE
-35 cat
-10 cat
cat
-35
-10
RNAI
-10
-35
T->A
ColEI Ext2 origin
RNAII Primer
Apa LI (3068)
replication start
-35 lacI
-10 lacI
Apa LI (2341)
lacI

pMx7 FS 5D2
4410 bp

Figure 12 (cont)

```
     XbaI    SphI
     ~~~~~~~~~~~~~
  1  TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
     AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA


 51  GGCACTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG
     CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC


              MfeI
              ~~~~~~~
101  ATGAAGTGCA ATTGGTGGAA AGCGGCGGCG GCCTGGTGCA ACCGGGCGGC
     TACTTCACGT TAACCACCTT TCGCCGCCGC CGGACCACGT TGGCCCGCCG


                        BspEI
                        ~~~~~~
151  AGCCTGCGTC TGAGCTGCGC GGCCTCCGGA TTTACCTTTA GCAGCTATGC
     TCGGACGCAG ACTCGACGCG CCGGAGGCCT AAATGGAAAT CGTCGATACG


                                  XhoI
                                  ~~~~~~
                                  AvaI
                                  ~~~~~~
201  GATGAGCTGG GTGCGCCAAG CCCCTGGGAA GGGTCTCGAG TGGGTGAGCG
     CTACTCGACC CACGCGGTTC GGGGACCCTT CCCAGAGCTC ACCCACTCGC


251  CGATTAGCGG TAGCGGCGGC AGCACCTATT ATGCGGATAG CGTGAAAGGC
     GCTAATCGCC ATCGCCGCCG TCGTGGATAA TACGCCTATC GCACTTTCCG


              BstBI
              ~~~~~~
              SfuI
              ~~~~~~
              NspV
              ~~~~~~
301  CGTTTTACCA TTTCACGTGA TAATTCGAAA AACACCCTGT ATCTGCAAAT
     GCAAAATGGT AAAGTGCACT ATTAAGCTTT TTGTGGGACA TAGACGTTTA


              EagI          BssHII
              ~~~~~~        ~~~~~~~
351  GAACAGCCTG CGTGCGGAAG ATACGGCCGT GTATTATTGC GCGCGTGTTA
     CTTGTCGGAC GCACGCCTTC TATGCCGGCA CATAATAACG CGCGCACAAT


                                            StyI
                                            ~~~~~~
401  AGAAGCATTT TTCTCGTAAG AATTGGTTTG ATTATTGGGG CCAAGGCACC
     TCTTCGTAAA AAGAGCATTC TTAACCAAAC TAATAACCCC GGTTCCGTGG
```

BlpI
~~~~~~~
CelII
~~~~~~

451   CTGGTGACGG TTAGCTCAGC GGGTGGCGGT TCTGGCGGCG GTGGGAGCGG
       GACCACTGCC AATCGAGTCG CCCACCGCCA AGACCGCCGC CACCCTCGCC

                                       EcoRV
                                      ~~~~~~~

501   TGGCGGTGGT TCTGGCGGTG GTGGTTCCGA TATCGTGATG ACCCAGAGCC
       ACCGCCACCA AGACCGCCAC CACCAAGGCT ATAGCACTAC TGGGTCTCGG

                                         PstI
                                        ~~~~~~

551   CACTGAGCCT GCCAGTGACT CCGGGCGAGC CTGCGAGCAT TAGCTGCAGA
       GTGACTCGGA CGGTCACTGA GGCCCGCTCG GACGCTCGTA ATCGACGTCT

                                         KpnI
                                        ~~~~
                                       Acc65I
                                        ~~~~

601   AGCAGCCAAA GCCTGCTGCA TAGCAACGGC TATAACTATC TGGATTGGTA
       TCGTCGGTTT CGGACGACGT ATCGTTGCCG ATATTGATAG ACCTAACCAT

KpnI
~~

Acc65I   SexAI
~~   ~~~~~~~~

651   CCTTCAAAAA CCAGGTCAAA GCCCGCAGCT ATTAATTTAT CTGGGCAGCA
       GGAAGTTTTT GGTCCAGTTT CGGGCGTCGA TAATTAAATA GACCCGTCGT

                                        BamHI
                                       ~~~~~~~

701   ACCGTGCCAG TGGGGTCCCG GATCGTTTTA GCGGCTCTGG ATCCGGCACC
       TGGCACGGTC ACCCCAGGGC CTAGCAAAAT CGCCGAGACC TAGGCCGTGG

                                        BpuAI
                                       ~~~~~~
                                       BbsI
                                       ~~~~~~

751   GATTTTACCC TGAAAATTAG CCGTGTGGAA GCTGAAGACG TGGGCGTGTA
       CTAAAATGGG ACTTTTAATC GGCACACCTT CGACTTCTGC ACCCGCACAT

                                        MscI
                                      ~~~~~~~

801   TTATTGCCAG CAGCATTATA CCACCCCGCC GACCTTTGGC CAGGGTACGA
       AATAACGGTC GTCGTAATAT GGTGGGGCGG CTGGAAACCG GTCCCATGCT

```
                        BsiWI  EcoRI
                        ~~~~~~~~~~~~~
   851  AAGTTGAAAT TAAACGTACG GAATTCGACT ATAAAGATGA CGATGACAAA
        TTCAACTTTA ATTTGCATGC CTTAAGCTGA TATTTCTACT GCTACTGTTT


              BssHII                            HindIII

              ~~~~~~                            ~~~~~~~
   901  GGCGCGCCGT GGAGCCACCC GCAGTTTGAA AAATGATAAG CTTGACCTGT
        CCGCGCGGCA CCTCGGTGGG CGTCAAACTT TTTACTATTC GAACTGGACA
                                                    OGIII3   100.0%

                                                    =======


   951  GAAGTGAAAA ATGGCGCAGA TTGTGCGACA TTTTTTTTGT CTGCCGTTTA
        CTTCACTTTT TACCGCGTCT AACACGCTGT AAAAAAAACA GACGGCAAAT
        OGIII3 100.0%

        ============


  1001  ATTAAAGGGG GGGGGGGGCC GGCCTGGGGG GGGGTGTACA TGAAATTGTA
        TAATTTCCCC CCCCCCCCGG CCGGACCCCC CCCCACATGT ACTTTAACAT

  1051  AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTGTT AAATCAGCTC
        TTGCAATTAT AAAACAATTT TAAGCGCAAT TTAAAAACAA TTTAGTCGAG

  1101  ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT AAATCAAAAG
        TAAAAAATTG GTTATCCGGC TTTAGCCGTT TTAGGGAATA TTTAGTTTTC

  1151  AATAGACCGA GATAGGGTTG AGTGTTGTTC CAGTTTGGAA CAAGAGTCCA
        TTATCTGGCT CTATCCCAAC TCACAACAAG GTCAAACCTT GTTCTCAGGT

  1201  CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA CCGTCTATCA
        GATAATTTCT TGCACCTGAG GTTGCAGTTT CCCGCTTTTT GGCAGATAGT

  1251  GGGCGATGGC CCACTACGAG AACCATCACC CTAATCAAGT TTTTTGGGGT
        CCCGCTACCG GGTGATGCTC TTGGTAGTGG GATTAGTTCA AAAAACCCCA

  1301  CGAGGTGCCG TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCGATTT
        GCTCCACGGC ATTTCGTGAT TTAGCCTTGG GATTTCCCTC GGGGGCTAAA

  1351  AGAGCTTGAC GGGGAAAGCC GGCGAACGTG GCGAGAAAGG AAGGGAAGAA
        TCTCGAACTG CCCCTTTCGG CCGCTTGCAC CGCTCTTTCC TTCCCTTCTT

  1401  AGCGAAAGGA GCGGGCGCTA GGGCGCTGGC AAGTGTAGCG GTCACGCTGC
        TCGCTTTCCT CGCCCGCGAT CCCGCGACCG TTCACATCGC CAGTGCGACG

  1451  GCGTAACCAC CACACCCGCC GCGCTTAATG CGCCGCTACA GGGCGCGTGC
        CGCATTGGTG GTGTGGGCGG CGCGAATTAC GCGGCGATGT CCCGCGCACG
```

Fig. 5 continued

```
1501   TAGACTAGTG TTTAAACCGG ACCGGGGGGG GGCTTAAGTG GGCTGCAAAA
       ATCTGATCAC AAATTTGGCC TGGCCCCCCC CCGAATTCAC CCGACGTTTT

1551   CAAAACGGCC TCCTGTCAGG AAGCCGCTTT TATCGGGTAG CCTCACTGCC
       GTTTTGCCGG AGGACAGTCC TTCGGCGAAA ATAGCCCATC GGAGTGACGG

1601   CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATCAG TGAATCGGCC
       GCGAAAGGTC AGCCCTTTGG ACAGCACGGT CGACGTAGTC ACTTAGCCGG

1651   AACGCGCGGG GAGAGGCGGT TTGCGTATTG GGAGCCAGGG TGGTTTTTCT
       TTGCGCGCCC CTCTCCGCCA AACGCATAAC CCTCGGTCCC ACCAAAAAGA

1701   TTTCACCAGT GAGACGGGCA ACAGCTGATT GCCCTTCACC GCCTGGCCCT
       AAAGTGGTCA CTCTGCCCGT TGTCGACTAA CGGGAAGTGG CGGACCGGGA

1751   GAGAGAGTTG CAGCAAGCGG TCCACGCTGG TTTGCCCCAG CAGGCGAAAA
       CTCTCTCAAC GTCGTTCGCC AGGTGCGACC AAACGGGGTC GTCCGCTTTT

1801   TCCTGTTTGA TGGTGGTCAG CGGCGGGATA TAACATGAGC TGTCCTCGGT
       AGGACAAACT ACCACCAGTC GCCGCCCTAT ATTGTACTCG ACAGGAGCCA

1851   ATCGTCGTAT CCCACTACCG AGATGTCCGC ACCAACGCGC AGCCCGGACT
       TAGCAGCATA GGGTGATGGC TCTACAGGCG TGGTTGCGCG TCGGGCCTGA

1901   CGGTAATGGC ACGCATTGCG CCCAGCGCCA TCTGATCGTT GGCAACCAGC
       GCCATTACCG TGCGTAACGC GGGTCGCGGT AGACTAGCAA CCGTTGGTCG

1951   ATCGCAGTGG GAACGATGCC CTCATTCAGC ATTTGCATGG TTTGTTGAAA
       TAGCGTCACC CTTGCTACGG GAGTAAGTCG TAAACGTACC AAACAACTTT

2001   ACCGGACATG GCACTCCAGT CGCCTTCCCG TTCCGCTATC GGCTGAATTT
       TGGCCTGTAC CGTGAGGTCA GCGGAAGGGC AAGGCGATAG CCGACTTAAA

2051   GATTGCGAGT GAGATATTTA TGCCAGCCAG CCAGACGCAG ACGCGCCGAG
       CTAACGCTCA CTCTATAAAT ACGGTCGGTC GGTCTGCGTC TGCGCGGCTC

2101   ACAGAACTTA ATGGGCCAGC TAACAGCGCG ATTTGCTGGT GGCCCAATGC
       TGTCTTGAAT TACCCGGTCG ATTGTCGCGC TAAACGACCA CCGGGTTACG

2151   GACCAGATGC TCCACGCCCA GTCGCGTACC GTCCTCATGG GAGAAAATAA
       CTGGTCTACG AGGTGCGGGT CAGCGCATGG CAGGAGTACC CTCTTTTATT

2201   TACTGTTGAT GGGTGTCTGG TCAGAGACAT CAAGAAATAA CGCCGGAACA
       ATGACAACTA CCCACAGACC AGTCTCTGTA GTTCTTTATT GCGGCCTTGT

2251   TTAGTGCAGG CAGCTTCCAC AGCAATAGCA TCCTGGTCAT CCAGCGGATA
       AATCACGTCC GTCGAAGGTG TCGTTATCGT AGGACCAGTA GGTCGCCTAT

                                                     ApaLI
                                                     ~~~~~~~
2301   GTTAATAATC AGCCCACTGA CACGTTGCGC GAGAAGATTG TGCACCGCCG
       CAATTATTAG TCGGGTGACT GTGCAACGCG CTCTTCTAAC ACGTGGCGGC

2351   CTTTACAGGC TTCGACGCCG CTTCGTTCTA CCATCGACAC GACCACGCTG
       GAAATGTCCG AAGCTGCGGC GAAGCAAGAT GGTAGCTGTG CTGGTGCGAC
```

FIGURE 5 cont'd

```
2401  GCACCCAGTT GATCGGCGCG AGATTTAATC GCCGCGACAA TTTGCGACGG
      CGTGGGTCAA CTAGCCGCGC TCTAAATTAG CGGCGCTGTT AAACGCTGCC

2451  CGCGTGCAGG GCCAGACTGG AGGTGGCAAC GCCAATCAGC AACGACTGTT
      GCGCACGTCC CGGTCTGACC TCCACCGTTG CGGTTAGTCG TTGCTGACAA

2501  TGCCCGCCAG TTGTTGTGCC ACGCGGTTAG GAATGTAATT CAGCTCCGCC
      ACGGGCGGTC AACAACACGG TGCGCCAATC CTTACATTAA GTCGAGGCGG

2551  ATCGCCGCTT CCACTTTTTC CCGCGTTTTC GCAGAAACGT GGCTGGCCTG
      TAGCGGCGAA GGTGAAAAAG GGCGCAAAAG CGTCTTTGCA CCGACCGGAC

2601  GTTCACCACG CGGGAAACGG TCTGATAAGA GACACCGGCA TACTCTGCGA
      CAAGTGGTGC GCCCTTTGCC AGACTATTCT CTGTGGCCGT ATGAGACGCT

2651  CATCGTATAA CGTTACTGGT TTCACATTCA CCACCCTGAA TTGACTCTCT
      GTAGCATATT GCAATGACCA AAGTGTAAGT GGTGGGACTT AACTGAGAGA

2701  TCCGGGCGCT ATCATGCCAT ACCGCGAAAG GTTTTGCGCC ATTCGATGCT
      AGGCCCGCGA TAGTACGGTA TGGCGCTTTC CAAAACGCGG TAAGCTACGA

2751  AGCCATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAGGCCG
      TCGGTACACT CGTTTTCCGG TCGTTTTCCG GTCCTTGGCA TTTTTCCGGC

2801  CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA
      GCAACGACCG CAAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT

2851  AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA
      TTAGCTGCGA GTTCAGTCTC CACCGCTTTG GGCTGTCCTG ATATTTCTAT

2901  CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC
      GGTCCGCAAA GGGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG

2951  TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG
      ACGGCGAATG GCCTATGGAC AGGCGGAAAG AGGGAAGCCC TTCGCACCGC

3001  CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG
      GAAAGAGTAT CGAGTGCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC

                        ApaLI
                        ~~~~~~~
3051  CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC GACCGCTGCG
      GAGGTTCGAC CCGACACACG TGCTTGGGGG GCAAGTCGGG CTGGCGACGC

3101  CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA
      GGAATAGGCC ATTGATAGCA GAACTCAGGT TGGGCCATTC TGTGCTGAAT

3151  TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT
      AGCGGTGACC GTCGTCGGTG ACCATTGTCC TAATCGTCTC GCTCCATACA

3201  AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA
      TCCGCCACGA TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT

3251  GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGTAGCCAGT TACCTTCGGA
      CTTCTTGTCA TAAACCATAG ACGCGAGACG ACATCGGTCA ATGGAAGCCT
```

FIG. 9-2 (cont.)

```
3301   AAAAGAGTTG  GTAGCTCTTG  ATCCGGCAAA  CAAACCACCG  CTGGTAGCGG
       TTTTCTCAAC  CATCGAGAAC  TAGGCCGTTT  GTTTGGTGGC  GACCATCGCC

3351   TGGTTTTTTT  GTTTGCAAGC  AGCAGATTAC  GCGCAGAAAA  AAAGGATCTC
       ACCAAAAAAA  CAAACGTTCG  TCGTCTAATG  CGCGTCTTTT  TTTCCTAGAG

3401   AAGAAGATCC  TTTGATCTTT  TCTACGGGGT  CTGACGCTCA  GTGGAACGAA
       TTCTTCTAGG  AAACTAGAAA  AGATGCCCCA  GACTGCGAGT  CACCTTGCTT

3451   AACTCACGTT  AAGGGATTTT  GGTCAGATCT  AGCACCAGGC  GTTTAAGGGC
       TTGAGTGCAA  TTCCCTAAAA  CCAGTCTAGA  TCGTGGTCCG  CAAATTCCCG

3501   ACCAATAACT  GCCTTAAAAA  AATTACGCCC  CGCCCTGCCA  CTCATCGCAG
       TGGTTATTGA  CGGAATTTTT  TTAATGCGGG  GCGGGACGGT  GAGTAGCGTC

3551   TACTGTTGTA  ATTCATTAAG  CATTCTGCCG  ACATGGAAGC  CATCACAAAC
       ATGACAACAT  TAAGTAATTC  GTAAGACGGC  TGTACCTTCG  GTAGTGTTTG

3601   GGCATGATGA  ACCTGAATCG  CCAGCGGCAT  CAGCACCTTG  TCGCCTTGCG
       CCGTACTACT  TGGACTTAGC  GGTCGCCGTA  GTCGTGGAAC  AGCGGAACGC

3651   TATAATATTT  GCCCATAGTG  AAAACGGGGG  CGAAGAAGTT  GTCCATATTG
       ATATTATAAA  CGGGTATCAC  TTTTGCCCCC  GCTTCTTCAA  CAGGTATAAC

3701   GCTACGTTTA  AATCAAAACT  GGTGAAACTC  ACCCAGGGAT  TGGCTGAGAC
       CGATGCAAAT  TTAGTTTTGA  CCACTTTGAG  TGGGTCCCTA  ACCGACTCTG

3751   GAAAAACATA  TTCTCAATAA  ACCCTTTAGG  GAAATAGGCC  AGGTTTTCAC
       CTTTTTGTAT  AAGAGTTATT  TGGGAAATCC  CTTTATCCGG  TCCAAAAGTG

3801   CGTAACACGC  CACATCTTGC  GAATATATGT  GTAGAAACTG  CCGGAAATCG
       GCATTGTGCG  GTGTAGAACG  CTTATATACA  CATCTTTGAC  GGCCTTTAGC

3851   TCGTGGTATT  CACTCCAGAG  CGATGAAAAC  GTTTCAGTTT  GCTCATGGAA
       AGCACCATAA  GTGAGGTCTC  GCTACTTTTG  CAAAGTCAAA  CGAGTACCTT

3901   AACGGTGTAA  CAAGGGTGAA  CACTATCCCA  TATCACCAGC  TCACCGTCTT
       TTGCCACATT  GTTCCCACTT  GTGATAGGGT  ATAGTGGTCG  AGTGGCAGAA

3951   TCATTGCCAT  ACGGAACTCC  GGGTGAGCAT  TCATCAGGCG  GCAAGAATG
       AGTAACGGTA  TGCCTTGAGG  CCCACTCGTA  AGTAGTCCGC  CCGTTCTTAC

4001   TGAATAAAGG  CCGGATAAAA  CTTGTGCTTA  TTTTTCTTTA  CGGTCTTTAA
       ACTTATTTCC  GGCCTATTTT  GAACACGAAT  AAAAAGAAAT  GCCAGAAATT

4051   AAAGGCCGTA  ATATCCAGCT  GAACGGTCTG  GTTATAGGTA  CATTGAGCAA
       TTTCCGGCAT  TATAGGTCGA  CTTGCCAGAC  CAATATCCAT  GTAACTCGTT

4101   CTGACTGAAA  TGCCTCAAAA  TGTTCTTTAC  GATGCCATTG  GGATATATCA
       GACTGACTTT  ACGGAGTTTT  ACAAGAAATG  CTACGGTAAC  CCTATATAGT

4151   ACGGTGGTAT  ATCCAGTGAT  TTTTTTCTCC  ATTTTAGCTT  CCTTAGCTCC
       TGCCACCATA  TAGGTCACTA  AAAAAAGAGG  TAAAATCGAA  GGAATCGAGG

4201   TGAAAATCTC  GATAACTCAA  AAAATACGCC  CGGTAGTGAT  CTTATTTCAT
       ACTTTTAGAG  CTATTGAGTT  TTTTATGCGG  GCCATCACTA  GAATAAAGTA
```

```
4251   TATGGTGAAA GTTGGAACCT CACCCGACGT CTAATGTGAG TTAGCTCACT
       ATACCACTTT CAACCTTGGA GTGGGCTGCA GATTACACTC AATCGAGTGA

4301   CATTAGGCAC CCCAGGCTTT ACACTTTATG CTTCCGGCTC GTATGTTGTG
       GTAATCCGTG GGGTCCGAAA TGTGAAATAC GAAGGCCGAG CATACAACAC

                                   M13 Reverse   primer   100.0%
                                   ==================
4351   TGGAATTGTG AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG
       ACCTTAACAC TCGCCTATTG TTAAAGTGTG TCCTTTGTCG ATACTGGTAC

4401   ATTACGAATT
       TAATGCTTAA
```

Figure 13

pMx9-Fab-GPC8
5020 bp

ompA - signal sequence
SD Seq
Xba I (4935)
M13 Reverse primer (100.0%)
SD SEQ
MRNA LAC OPERON
LAC OPERATOR
-10
-35
deletion of T
CAP SITE
-35 cat
-10 cat
cat
-35
-10
RNAI
-10
-35
T->A
ColEI Ext2 origin
RNAII Primer
Apa LI (3591)
replication start
-35 lacI
-10 lacI
Apa LI (2864)
lacI

Eco RV (1)
Sex AI (37)
Acc 65I (105)
Kpn I (109)
Xma I (119)
Ava I (119)
Sma I (121)
Bsu 36I (166)
Bam H I (191)
Bbs I (249)
Bpu AI (249)
Bsu 36I (282)
Msc I (325)
Dra III (345)
CL lambda
Stu I (636)
Sph I (649)
SD SEQ
pho A
Mfe I (735)
Rsp EI (801)
Xho I (867)
Ava I (867)
Nsp V (954)
Sfu I (954)
Bst BI (954)
Bss HII (1018)
Sty I (1061)
Cel II (1085)
Blp I (1085)
CH1
Eco R I (1395)
Flagtag
FLAG (M2)
Bss HII (1426)
Streptagll
Hin d III (1462)
OGIII3 (100.0%)
functional ssori
GenI-Nick
T->G
G->C
recognition stemloop
Insert GGCCTTTTGCT

Figure 13 (cont)

```
     EcoRV                                              SexAI
     ~~~                                                ~~~~~~~~
  1  ATCGTGCTGA CCCAGCCGCC TTCAGTGAGT GGCGCACCAG GTCAGCGTGT
     TAGCACGACT GGGTCGGCGG AAGTCACTCA CCGCGTGGTC CAGTCGCACA


 51  GACCATCTCG TGTAGCGGCA GCAGCAGCAA CATTGGCAGC AACTATGTGA
     CTGGTAGAGC ACATCGCCGT CGTCGTCGTT GTAACCGTCG TTGATACACT


                     XmaI
                     ~~~~~~~
          KpnI       SmaI
          ~~~~~~     ~~~~~~~
          Acc65I     AvaI
          ~~~~~~     ~~~~~~
101  GCTGGTACCA GCAGTTGCCC GGGACGGCGC CGAAACTGCT GATTTATGAT
     CGACCATGGT CGTCAACGGG CCCTGCCGCG GCTTTGACGA CTAAATACTA


                 Bsu36I                          BamHI
                 ~~~~~~~                          ~~~~~~~
151  AACAACCAGC GTCCCTCAGG CGTGCCGGAT CGTTTTAGCG GATCCAAAAG
     TTGTTGGTCG CAGGGAGTCC GCACGGCCTA GCAAAATCGC CTAGGTTTTC


                                                 BpuAI
                                                 ~~~~~~
                                                 BbsI
                                                 ~~~~~~
201  CGGCACCAGC GCGAGCCTTG CGATTACGGG CCTGCAAAGC GAAGACGAAG
     GCCGTGGTCG CGCTCGGAAC GCTAATGCCC GGACGTTTCG CTTCTGCTTC


                                     Bsu36I
                                     ~~~~~~~~
251  CGGATTATTA TTGCCAGAGC TATGACATGC CTCAGGCTGT GTTTGGCGGC
     GCCTAATAAT AACGGTCTCG ATACTGTACG GAGTCCGACA CAAACCGCCG


                         MscI            DraIII
                         ~~~~~~          ~~~~~~~~~~
301  GGCACGAAGT TTAACCGTTC TTGGCCAGCC GAAAGCCGCA CCGAGTGTGA
     CCGTGCTTCA AATTGGCAAG AACCGGTCGG CTTTCGGCGT GGCTCACACT


351  CGCTGTTTCC GCCGAGCAGC GAAGAATTGC AGGCGAACAA AGCGACCCTG
     GCGACAAAGG CGGCTCGTCG CTTCTTAACG TCCGCTTGTT TCGCTGGGAC


401  GTGTGCCTGA TTAGCGACTT TTATCCGGGA GCCGTGACAG TGGCCTGGAA
     CACACGGACT AATCGCTGAA AATAGGCCCT CGGCACTGTC ACCGGACCTT


451  GGCAGATAGC AGCCCCGTCA AGGCGGGAGT GGAGACCACC ACACCCTCCA
     CCGTCTATCG TCGGGGCAGT TCCGCCCTCA CCTCTGGTGG TGTGGGAGGT


501  AACAAAGCAA CAACAAGTAC GCGGCCAGCA GCTATCTGAG CCTGACGCCT
     TTGTTTCGTT GTTGTTCATG CGCCGGTCGT CGATAGACTC GGACTGCGGA


551  GAGCAGTGGA AGTCCCACAG AAGCTACAGC TGCCAGGTCA CGCATGAGGG
     CTCGTCACCT TCAGGGTGTC TTCGATGTCG ACGGTCCAGT GCGTACTCCC

                                            StuI       SphI
```
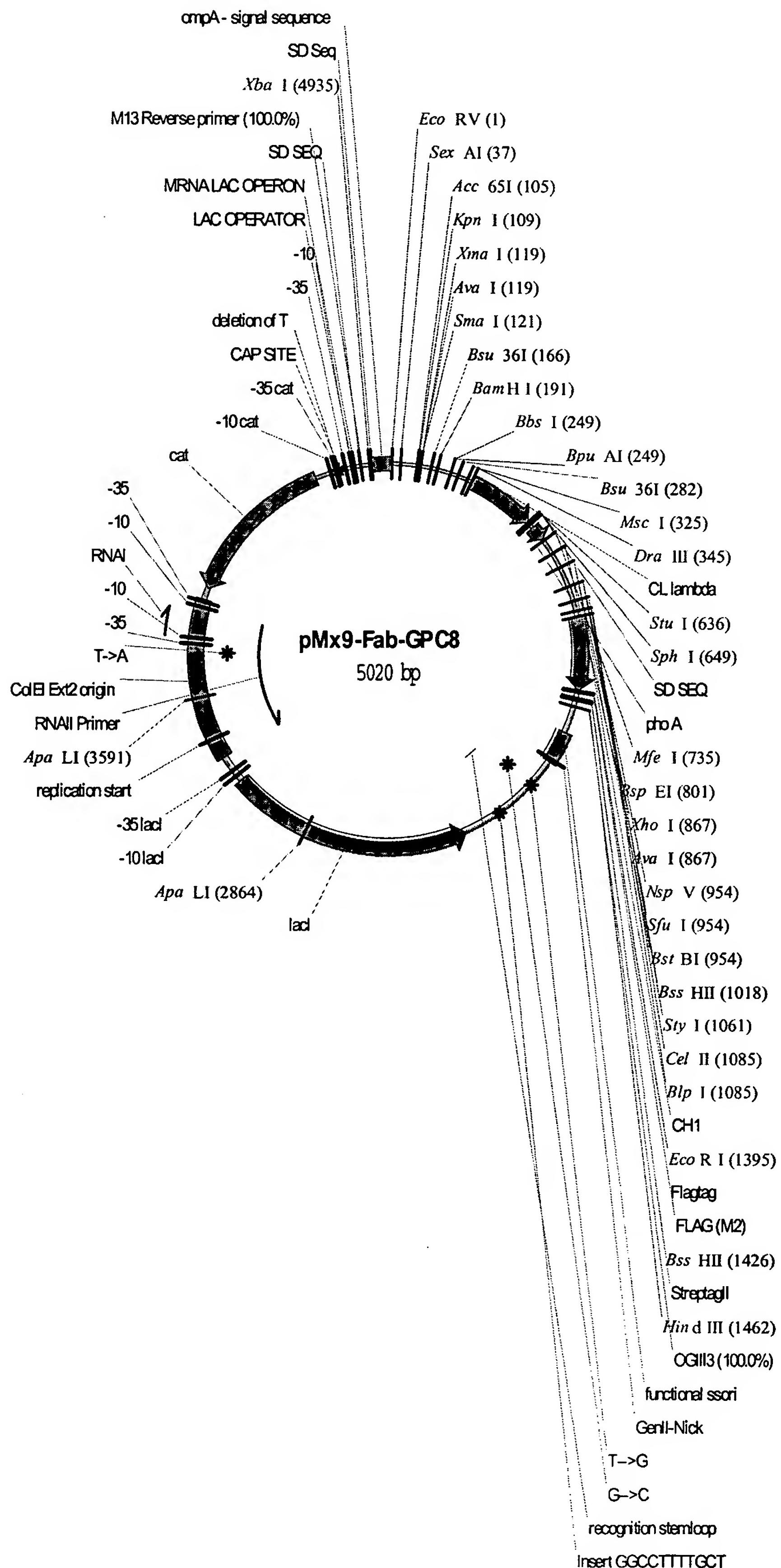
```
                                                    ~~~~~~        ~~~~~~
601  GAGCACCGTG GAAAAAACCG TTGCGCCGAC TGAGGCCTGA TAAGCATGCG
     CTCGTGGCAC CTTTTTTGGC AACGCGGCTG ACTCCGGACT ATTCGTACGC

651  TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC ACTCTTACCG
     ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG TGAGAATGGC

                                                    MfeI
                                                    ~~~~~~
701  TTGCTCTTCA CCCCTGTTAC CAAAGCCCAG GTGCAATTGA AAGAAAGCGG
     AACGAGAAGT GGGGACAATG GTTTCGGGTC CACGTTAACT TTCTTTCGCC

                                                          BspEI
                                                          ~
751  CCCGGCCCTG GTGAAACCGA CCCAAACCCT GACCCTGACC TGTACCTTTT
     GGGCCGGGAC CACTTTGGCT GGGTTTGGGA CTGGGACTGG ACATGGAAAA

     BspEI
     ~~~~~
801  CCGGATTTAG CCTGTCCACG TCTGGCGTTG GCGTGGGCTG GATTCGCCAG
     GGCCTAAATC GGACAGGTGC AGACCGCAAC CGCACCCGAC CTAAGCGGTC

                     XhoI
                     ~~~~~~~
                     AvaI
                     ~~~~~~~
851  CCGCCTGGGA AAGCCCTCGA GTGGCTGGCT CTGATTGATT GGGATGATGA
     GGCGGACCCT TTCGGGAGCT CACCGACCGA GACTAACTAA CCCTACTACT

901  TAAGTATTAT AGCACCAGCC TGAAAACGCG TCTGACCATT AGCAAAGATA
     ATTCATAATA TCGTGGTCGG ACTTTTGCGC AGACTGGTAA TCGTTTCTAT

        BstBI
        ~~~~~~
        SfuI
        ~~~~~~
        NspV
        ~~~~~~
951  CTTCGAAAAA TCAGGTGGTG CTGACTATGA CCAACATGGA CCCGGTGGAT
     GAAGCTTTTT AGTCCACCAC GACTGATACT GGTTGTACCT GGGCCACCTA

                     BssHII
                     ~~~~~~~
1001 ACGGCCACCT ATTATTGCGC GCGTTCTCCT CGTTATCGTG GTGCTTTTGA
     TGCCGGTGGA TAATAACGCG CGCAAGAGGA GCAATAGCAC CACGAAAACT

                                        BlpI
                                        ~~~~~~~
                     StyI               CelII
                     ~~~~~~~            ~~~~~~~
1051 TTATTGGGGC CAAGGCACCC TGGTGACGGT TAGCTCAGCG TCGACCAAAG
     AATAACCCCG GTTCCGTGGG ACCACTGCCA ATCGAGTCGC AGCTGGTTTC

1101 GTCCAAGCGT GTTTCCGCTG GCTCCGAGCA GCAAAAGCAC CAGCGGCGGC
     CAGGTTCGCA CAAAGGCGAC CGAGGCTCGT CGTTTTCGTG GTCGCCGCCG

1151 ACGGCTGCCC TGGGCTGCCT GGTTAAAGAT TATTTCCCGG AACCAGTCAC
```

```
              TGCCGACGGG ACCCGACGGA CCAATTTCTA ATAAAGGGCC TTGGTCAGTG

        1201  CGTGAGCTGG AACAGCGGGG CGCTGACCAG CGGCGTGCAT ACCTTTCCGG
              GCACTCGACC TTGTCGCCCC GCGACTGGTC GCCGCACGTA TGGAAAGGCC

        1251  CGGTGCTGCA AAGCAGCGGC CTGTATAGCC TGAGCAGCGT TGTGACCGTG
              GCCACGACGT TTCGTCGCCG GACATATCGG ACTCGTCGCA ACACTGGCAC

        1301  CCGAGCAGCA GCTTAGGCAC TCAGACCTAT ATTTGCAACG TGAACCATAA
              GGCTCGTCGT CGAATCCGTG AGTCTGGATA TAAACGTTGC ACTTGGTATT

                                                            EcoRI
                                                            ~~~~~~
        1351  ACCGAGCAAC ACCAAAGTGG ATAAAAAGT GGAACCGAAA AGCGAATTCG
              TGGCTCGTTG TGGTTTCACC TATTTTTTCA CCTTGGCTTT TCGCTTAAGC

                                         BssHII
                                         ~~~~~~
        1401  ACTATAAAGA TGACGATGAC AAAGGCGCGC CGTGGAGCCA CCCGCAGTTT
              TGATATTTCT ACTGCTACTG TTTCCGCGCG GCACCTCGGT GGGCGTCAAA

                             HindIII
                             ~~~~~~
        1451  GAAAAATGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
              CTTTTTACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                             OGIII3   100.0%
                             ====================
        1501  ACATTTTTTT TGTCTGCCGT TTAATTAAAG GGGGGGGGGG GCCGGCCTGG
              TGTAAAAAAA ACAGACGGCA AATTAATTTC CCCCCCCCCC CGGCCGGACC

        1551  GGGGGGGTGT ACATGAAATT GTAAACGTTA ATATTTTGTT AAAATTCGCG
              CCCCCCCACA TGTACTTTAA CATTTGCAAT TATAAAACAA TTTTAAGCGC

        1601  TTAAATTTTT GTTAAATCAG CTCATTTTTT AACCAATAGG CCGAAATCGG
              AATTTAAAAA CAATTTAGTC GAGTAAAAAA TTGGTTATCC GGCTTTAGCC

        1651  CAAAATCCCT TATAAATCAA AAGAATAGAC CGAGATAGGG TTGAGTGTTG
              GTTTTAGGGA ATATTTAGTT TTCTTATCTG GCTCTATCCC AACTCACAAC

        1701  TTCCAGTTTG GAACAAGAGT CCACTATTAA AGAACGTGGA CTCCAACGTC
              AAGGTCAAAC CTTGTTCTCA GGTGATAATT TCTTGCACCT GAGGTTGCAG

        1751  AAAGGGCGAA AAACCGTCTA TCAGGGCGAT GGCCCACTAC GAGAACCATC
              TTTCCCGCTT TTTGGCAGAT AGTCCCGCTA CCGGGTGATG CTCTTGGTAG

        1801  ACCCTAATCA AGTTTTTTGG GGTCGAGGTG CCGTAAAGCA CTAAATCGGA
              TGGGATTAGT TCAAAAAACC CCAGCTCCAC GGCATTTCGT GATTTAGCCT

        1851  ACCCTAAAGG GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC
              TGGGATTTCC CTCGGGGGCT AAATCTCGAA CTGCCCCTTT CGGCCGCTTG

        1901  GTGGCGAGAA AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT
              CACCGCTCTT TCCTTCCCTT CTTTCGCTTT CCTCGCCCGC GATCCCGCGA

        1951  GGCAAGTGTA GCGGTCACGC TGCGCGTAAC CACCACACCC GCCGCGCTTA
              CCGTTCACAT CGCCAGTGCG ACGCGCATTG GTGGTGTGGG CGGCGCGAAT
```

```
2001  ATGCGCCGCT ACAGGGCGCG TGCTAGACTA GTGTTTAAAC CGGACCGGGG
      TACGCGGCGA TGTCCCGCGC ACGATCTGAT CACAAATTTG GCCTGGCCCC

2051  GGGGGCTTAA GTGGGCTGCA AAACAAAACG GCCTCCTGTC AGGAAGCCGC
      CCCCCGAATT CACCCGACGT TTTGTTTTGC CGGAGGACAG TCCTTCGGCG

2101  TTTTATCGGG TAGCCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG
      AAAATAGCCC ATCGGAGTGA CGGGCGAAAG GTCAGCCCTT TGGACAGCAC

2151  CCAGCTGCAT CAGTGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA
      GGTCGACGTA GTCACTTAGC CGGTTGCGCG CCCCTCTCCG CCAAACGCAT

2201  TTGGGAGCCA GGGTGGTTTT TCTTTTCACC AGTGAGACGG GCAACAGCTG
      AACCCTCGGT CCCACCAAAA AGAAAAGTGG TCACTCTGCC CGTTGTCGAC

2251  ATTGCCCTTC ACCGCCTGGC CCTGAGAGAG TTGCAGCAAG CGGTCCACGC
      TAACGGGAAG TGGCGGACCG GGACTCTCTC AACGTCGTTC GCCAGGTGCG

2301  TGGTTTGCCC CAGCAGGCGA AAATCCTGTT TGATGGTGGT CAGCGGCGGG
      ACCAAACGGG GTCGTCCGCT TTTAGGACAA ACTACCACCA GTCGCCGCCC

2351  ATATAACATG AGCTGTCCTC GGTATCGTCG TATCCCACTA CCGAGATGTC
      TATATTGTAC TCGACAGGAG CCATAGCAGC ATAGGGTGAT GGCTCTACAG

2401  CGCACCAACG CGCAGCCCGG ACTCGGTAAT GGCACGCATT GCGCCCAGCG
      GCGTGGTTGC GCGTCGGGCC TGAGCCATTA CCGTGCGTAA CGCGGGTCGC

2451  CCATCTGATC GTTGGCAACC AGCATCGCAG TGGGAACGAT GCCCTCATTC
      GGTAGACTAG CAACCGTTGG TCGTAGCGTC ACCCTTGCTA CGGGAGTAAG

2501  AGCATTTGCA TGGTTTGTTG AAAACCGGAC ATGGCACTCC AGTCGCCTTC
      TCGTAAACGT ACCAAACAAC TTTTGGCCTG TACCGTGAGG TCAGCGGAAG

2551  CCGTTCCGCT ATCGGCTGAA TTTGATTGCG AGTGAGATAT TTATGCCAGC
      GGCAAGGCGA TAGCCGACTT AAACTAACGC TCACTCTATA AATACGGTCG

2601  CAGCCAGACG CAGACGCGCC GAGACAGAAC TTAATGGGCC AGCTAACAGC
      GTCGGTCTGC GTCTGCGCGG CTCTGTCTTG AATTACCCGG TCGATTGTCG

2651  GCGATTTGCT GGTGGCCCAA TGCGACCAGA TGCTCCACGC CCAGTCGCGT
      CGCTAAACGA CCACCGGGTT ACGCTGGTCT ACGAGGTGCG GGTCAGCGCA

2701  ACCGTCCTCA TGGGAGAAAA TAATACTGTT GATGGGTGTC TGGTCAGAGA
      TGGCAGGAGT ACCCTCTTTT ATTATGACAA CTACCCACAG ACCAGTCTCT

2751  CATCAAGAAA TAACGCCGGA ACATTAGTGC AGGCAGCTTC CACAGCAATA
      GTAGTTCTTT ATTGCGGCCT TGTAATCACG TCCGTCGAAG GTGTCGTTAT

2801  GCATCCTGGT CATCCAGCGG ATAGTTAATA ATCAGCCCAC TGACACGTTG
      CGTAGGACCA GTAGGTCGCC TATCAATTAT TAGTCGGGTG ACTGTGCAAC

                      ApaLI
                      ~~~~~~
2851  CGCGAGAAGA TTGTGCACCG CCGCTTTACA GGCTTCGACG CCGCTTCGTT
      GCGCTCTTCT AACACGTGGC GGCGAAATGT CCGAAGCTGC GGCGAAGCAA
```

```
2901   CTACCATCGA CACGACCACG CTGGCACCCA GTTGATCGGC GCGAGATTTA
       GATGGTAGCT GTGCTGGTGC GACCGTGGGT CAACTAGCCG CGCTCTAAAT

2951   ATCGCCGCGA CAATTTGCGA CGGCGCGTGC AGGGCCAGAC TGGAGGTGGC
       TAGCGGCGCT GTTAAACGCT GCCGCGCACG TCCCGGTCTG ACCTCCACCG

3001   AACGCCAATC AGCAACGACT GTTTGCCCGC CAGTTGTTGT GCCACGCGGT
       TTGCGGTTAG TCGTTGCTGA CAAACGGGCG GTCAACAACA CGGTGCGCCA

3051   TAGGAATGTA ATTCAGCTCC GCCATCGCCG CTTCCACTTT TTCCCGCGTT
       ATCCTTACAT TAAGTCGAGG CGGTAGCGGC GAAGGTGAAA AAGGGCGCAA

3101   TTCGCAGAAA CGTGGCTGGC CTGGTTCACC ACGCGGGAAA CGGTCTGATA
       AAGCGTCTTT GCACCGACCG GACCAAGTGG TGCGCCCTTT GCCAGACTAT

3151   AGAGACACCG GCATACTCTG CGACATCGTA TAACGTTACT GGTTTCACAT
       TCTCTGTGGC CGTATGAGAC GCTGTAGCAT ATTGCAATGA CCAAAGTGTA

3201   TCACCACCCT GAATTGACTC TCTTCCGGGC GCTATCATGC CATACCGCGA
       AGTGGTGGGA CTTAACTGAG AGAAGGCCCG CGATAGTACG GTATGGCGCT

3251   AAGGTTTTGC GCCATTCGAT GCTAGCCATG TGAGCAAAAG GCCAGCAAAA
       TTCCAAAACG CGGTAAGCTA CGATCGGTAC ACTCGTTTTC CGGTCGTTTT

3301   GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC
       CCGGTCCTTG GCATTTTTCC GGCGCAACGA CCGCAAAAAG GTATCCGAGG

3351   GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA
       CGGGGGGACT GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT CTCCACCGCT

3401   AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT
       TTGGGCTGTC CTGATATTTC TATGGTCCGC AAAGGGGGAC CTTCGAGGGA

3451   CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT
       GCACGCGAGA GGACAAGGCT GGGACGGCGA ATGGCCTATG GACAGGCGGA

3501   TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC ATAGCTCACG CTGTAGGTAT
       AAGAGGGAAG CCCTTCGCAC CGCGAAAGAG TATCGAGTGC GACATCCATA

                                                    ApaLI
                                                    ~~~~~~~
3551   CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
       GAGTCAAGCC ACATCCAGCA AGCGAGGTTC GACCCGACAC ACGTGCTTGG

3601   CCCCGTTCAG CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT
       GGGGCAAGTC GGGCTGGCGA CGCGGAATAG GCCATTGATA GCAGAACTCA

3651   CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC
       GGTTGGGCCA TTCTGTGCTG AATAGCGGTG ACCGTCGTCG GTGACCATTG

3701   AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG
       TCCTAATCGT CTCGCTCCAT ACATCCGCCA CGATGTCTCA AGAACTTCAC

3751   GTGGCCTAAC TACGGCTACA CTAGAAGAAC AGTATTTGGT ATCTGCGCTC
       CACCGGATTG ATGCCGATGT GATCTTCTTG TCATAAACCA TAGACGCGAG

3801   TGCTGTAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC
```

```
              ACGACATCGG TCAATGGAAG CCTTTTTCTC AACCATCGAG AACTAGGCCG

3851  AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT
      TTTGTTTGGT GGCGACCATC GCCACCAAAA AAACAAACGT TCGTCGTCTA

3901  TACGCGCAGA AAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG
      ATGCGCGTCT TTTTTTCCTA GAGTTCTTCT AGGAAACTAG AAAAGATGCC

3951  GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCAGA
      CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA AAACCAGTCT

4001  TCTAGCACCA GGCGTTTAAG GGCACCAATA ACTGCCTTAA AAAAATTACG
      AGATCGTGGT CCGCAAATTC CCGTGGTTAT TGACGGAATT TTTTTAATGC

4051  CCCCGCCCTG CCACTCATCG CAGTACTGTT GTAATTCATT AAGCATTCTG
      GGGGCGGGAC GGTGAGTAGC GTCATGACAA CATTAAGTAA TTCGTAAGAC

4101  CCGACATGGA AGCCATCACA AACGGCATGA TGAACCTGAA TCGCCAGCGG
      GGCTGTACCT TCGGTAGTGT TTGCCGTACT ACTTGGACTT AGCGGTCGCC

4151  CATCAGCACC TTGTCGCCTT GCGTATAATA TTTGCCCATA GTGAAAACGG
      GTAGTCGTGG AACAGCGGAA CGCATATTAT AAACGGGTAT CACTTTTGCC

4201  GGGCGAAGAA GTTGTCCATA TTGGCTACGT TTAAATCAAA ACTGGTGAAA
      CCCGCTTCTT CAACAGGTAT AACCGATGCA AATTTAGTTT TGACCACTTT

4251  CTCACCCAGG GATTGGCTGA GACGAAAAAC ATATTCTCAA TAAACCCTTT
      GAGTGGGTCC CTAACCGACT CTGCTTTTTG TATAAGAGTT ATTTGGGAAA

4301  AGGGAAATAG GCCAGGTTTT CACCGTAACA CGCCACATCT TGCGAATATA
      TCCCTTTATC CGGTCCAAAA GTGGCATTGT GCGGTGTAGA ACGCTTATAT

4351  TGTGTAGAAA CTGCCGGAAA TCGTCGTGGT ATTCACTCCA GAGCGATGAA
      ACACATCTTT GACGGCCTTT AGCAGCACCA TAAGTGAGGT CTCGCTACTT

4401  AACGTTTCAG TTTGCTCATG GAAAACGGTG TAACAAGGGT GAACACTATC
      TTGCAAAGTC AAACGAGTAC CTTTTGCCAC ATTGTTCCCA CTTGTGATAG

4451  CCATATCACC AGCTCACCGT CTTTCATTGC CATACGGAAC TCCGGGTGAG
      GGTATAGTGG TCGAGTGGCA GAAAGTAACG GTATGCCTTG AGGCCCACTC

4501  CATTCATCAG GCGGGCAAGA ATGTGAATAA AGGCCGGATA AAACTTGTGC
      GTAAGTAGTC CGCCCGTTCT TACACTTATT TCCGGCCTAT TTTGAACACG

4551  TTATTTTTCT TTACGGTCTT TAAAAAGGCC GTAATATCCA GCTGAACGGT
      AATAAAAAGA AATGCCAGAA ATTTTTCCGG CATTATAGGT CGACTTGCCA

4601  CTGGTTATAG GTACATTGAG CAACTGACTG AAATGCCTCA AAATGTTCTT
      GACCAATATC CATGTAACTC GTTGACTGAC TTTACGGAGT TTTACAAGAA

4651  TACGATGCCA TTGGGATATA TCAACGGTGG TATATCCAGT GATTTTTTTC
      ATGCTACGGT AACCCTATAT AGTTGCCACC ATATAGGTCA CTAAAAAAAG

4701  TCCATTTTAG CTTCCTTAGC TCCTGAAAAT CTCGATAACT CAAAAAATAC
      AGGTAAAATC GAAGGAATCG AGGACTTTTA GAGCTATTGA GTTTTTTATG

4751  GCCCGGTAGT GATCTTATTT CATTATGGTG AAAGTTGGAA CCTCACCCGA
```

```
      CGGGCCATCA CTAGAATAAA GTAATACCAC TTTCAACCTT GGAGTGGGCT

4801  CGTCTAATGT GAGTTAGCTC ACTCATTAGG CACCCCAGGC TTTACACTTT
      GCAGATTACA CTCAATCGAG TGAGTAATCC GTGGGGTCCG AAATGTGAAA

4851  ATGCTTCCGG CTCGTATGTT GTGTGGAATT GTGAGCGGAT AACAATTTCA
      TACGAAGGCC GAGCATACAA CACACCTTAA CACTCGCCTA TTGTTAAAGT

      M13 Reverse  primer 100.0%              XbaI
      ==================                     ~~~~~~
4901  CACAGGAAAC AGCTATGACC ATGATTACGA ATTTCTAGAT AACGAGGGCA
      GTGTCCTTTG TCGATACTGG TACTAATGCT TAAAGATCTA TTGCTCCCGT

4951  AAAAATGAAA AAGACAGCTA TCGCGATTGC AGTGGCACTG GCTGGTTTCG
      TTTTTACTTT TTCTGTCGAT AGCGCTAACG TCACCGTGAC CGACCAAAGC

                   EcoRV
                   ~~~
5001  CTACCGTAGC GCAGGCCGAT
      GATGGCATCG CGTCCGGCTA
```

Figure 14

pMorph18-Fab-GPC8
4145 bp

M13 Reverse primer (100.0%)
SD SEQ
LAC OPERATOR
MRNA LAC OPERON
-10
-35
CAP SITE
-35 cat
-10 cat
cat
-35
-10
RNAI
-10
-35
T->A
ColEI Ext2 origin
Apa LI (2803)
recognition stemloop
f1 origin
GenII-Nick

Eco RV (87)
Sex AI (123)
Acc 65I (191)
Kpn I (195)
Xma I (205)
Ava I (205)
Sma I (207)
Bsu 36I (252)
BamH I (277)
Bbs I (335)
Bpu AI (335)
Bsu 36I (368)
Msc I (411)
Dra III (431)
Stu I (722)
Sph I (735)
Mfe I (821)
Bsp EI (887)
Xho I (953)
Ava I (953)
Nsp V (1040)
Sfu I (1040)
Bst BI (1040)
Bss HII (1104)
Sty I (1147)
Cel II (1171)
Blp I (1171)
Eco R I (1481)
gIIIseq9 (100.0%)
Cla I (1635)
A->C
gIIIss
A->C
C->A
Hind III (1962)
OGIII3 (100.0%)

Figure 14 (cont)

```
  1  TCAGATAACG AGGGCAAAAA ATGAAAAAGA CAGCTATCGC GATTGCAGTG
     AGTCTATTGC TCCCGTTTTT TACTTTTTCT GTCGATAGCG CTAACGTCAC


                                             EcoRV
                                             ~~~~~~
 51  GCACTGGCTG GTTTCGCTAC CGTAGCGCAG GCCGATATCG TGCTGACCCA
     CGTGACCGAC CAAAGCGATG GCATCGCGTC CGGCTATAGC ACGACTGGGT


                          SexAI
                          ~~~~~~~
101  GCCGCCTTCA GTGAGTGGCG CACCAGGTCA GCGTGTGACC ATCTCGTGTA
     CGGCGGAAGT CACTCACCGC GTGGTCCAGT CGCACACTGG TAGAGCACAT


                                                     KpnI
                                                     ~~~~~~~
                                                     Acc65I
                                                     ~~~~~~~
151  GCGGCAGCAG CAGCAACATT GGCAGCAACT ATGTGAGCTG GTACCAGCAG
     CGCCGTCGTC GTCGTTGTAA CCGTCGTTGA TACACTCGAC CATGGTCGTC


         XmaI
         ~~~~~~
         SmaI
         ~~~~~~
         AvaI                                          Bsu36I
         ~~~~~~                                            ~
201  TTGCCCGGGA CGGCGCCGAA ACTGCTGATT TATGATAACA ACCAGCGTCC
     AACGGGCCCT GCCGCGGCTT TGACGACTAA ATACTATTGT TGGTCGCAGG


     Bsu36I                        BamHI
     ~~~~~~                        ~~~~~~~
251  CTCAGGCGTG CCGGATCGTT TTAGCGGATC CAAAAGCGGC ACCAGCGCGA
     GAGTCCGCAC GGCCTAGCAA AATCGCCTAG GTTTTCGCCG TGGTCGCGCT


                                     BpuAI
                                     ~~~~~~~
                                     BbsI
                                     ~~~~~~~
301  GCCTTGCGAT TACGGGCCTG CAAAGCGAAG ACGAAGCGGA TTATTATTGC
     CGGAACGCTA ATGCCCGGAC GTTTCGCTTC TGCTTCGCCT AATAATAACG


                       Bsu36I
                       ~~~~~~~~
351  CAGAGCTATG ACATGCCTCA GGCTGTGTTT GGCGGCGGCA CGAAGTTTAA
     GTCTCGATAC TGTACGGAGT CCGACACAAA CCGCCGCCGT GCTTCAAATT


              MscI              DraIII
              ~~~~~~~           ~~~~~~~~~~
401  CCGTTCTTGG CCAGCCGAAA GCCGCACCGA GTGTGACGCT GTTTCCGCCG
     GGCAAGAACC GGTCGGCTTT CGGCGTGGCT CACACTGCGA CAAAGGCGGC


451  AGCAGCGAAG AATTGCAGGC GAACAAAGCG ACCCTGGTGT GCCTGATTAG
     TCGTCGCTTC TTAACGTCCG CTTGTTTCGC TGGGACCACA CGGACTAATC


501  CGACTTTTAT CCGGGAGCCG TGACAGTGGC CTGGAAGGCA GATAGCAGCC
```
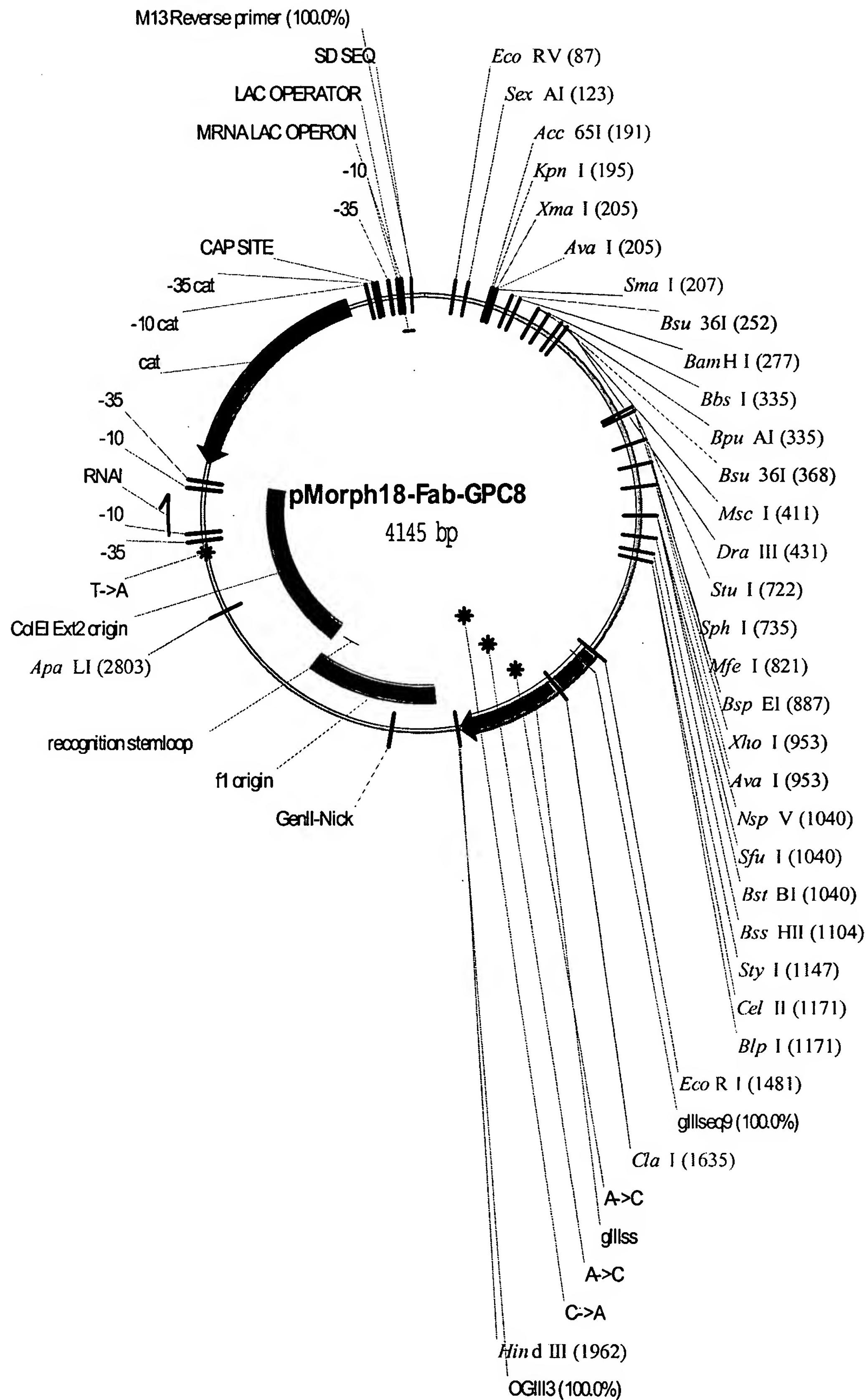
```
        GCTGAAAATA GGCCCTCGGC ACTGTCACCG GACCTTCCGT CTATCGTCGG

 551    CCGTCAAGGC GGGAGTGGAG ACCACCACAC CCTCCAAACA AAGCAACAAC
        GGCAGTTCCG CCCTCACCTC TGGTGGTGTG GGAGGTTTGT TTCGTTGTTG

 601    AAGTACGCGG CCAGCAGCTA TCTGAGCCTG ACGCCTGAGC AGTGGAAGTC
        TTCATGCGCC GGTCGTCGAT AGACTCGGAC TGCGGACTCG TCACCTTCAG

 651    CCACAGAAGC TACAGCTGCC AGGTCACGCA TGAGGGGAGC ACCGTGGAAA
        GGTGTCTTCG ATGTCGACGG TCCAGTGCGT ACTCCCCTCG TGGCACCTTT

                       StuI              SphI
                    ~~~~~~~           ~~~~~~~
 701    AAACCGTTGC GCCGACTGAG GCCTGATAAG CATGCGTAGG AGAAAATAAA
        TTTGGCAACG CGGCTGACTC CGGACTATTC GTACGCATCC TCTTTTATTT

 751    ATGAAACAAA GCACTATTGC ACTGGCACTC TTACCGTTGC TCTTCACCCC
        TACTTTGTTT CGTGATAACG TGACCGTGAG AATGGCAACG AGAAGTGGGG

                       MfeI
                    ~~~~~~~
 801    TGTTACCAAA GCCCAGGTGC AATTGAAAGA AAGCGGCCCG GCCCTGGTGA
        ACAATGGTTT CGGGTCCACG TTAACTTTCT TTCGCCGGGC CGGGACCACT

                                            BspEI
                                         ~~~~~~~
 851    AACCGACCCA AACCCTGACC CTGACCTGTA CCTTTTCCGG ATTTAGCCTG
        TTGGCTGGGT TTGGGACTGG GACTGGACAT GGAAAAGGCC TAAATCGGAC

 901    TCCACGTCTG GCGTTGGCGT GGGCTGGATT CGCCAGCCGC CTGGGAAAGC
        AGGTGCAGAC CGCAACCGCA CCCGACCTAA GCGGTCGGCG GACCCTTTCG

        XhoI
     ~~~~~~~
        AvaI
     ~~~~~~
 951    CCTCGAGTGG CTGGCTCTGA TTGATTGGGA TGATGATAAG TATTATAGCA
        GGAGCTCACC GACCGAGACT AACTAACCCT ACTACTATTC ATAATATCGT

                                            BstBI
                                         ~~~~~~~
                                            SfuI
                                         ~~~~~~~
                                            NspV
                                         ~~~~~~~
1001    CCAGCCTGAA AACGCGTCTG ACCATTAGCA AAGATACTTC GAAAAATCAG
        GGTCGGACTT TTGCGCAGAC TGGTAATCGT TTCTATGAAG CTTTTTAGTC

1051    GTGGTGCTGA CTATGACCAA CATGGACCCG GTGGATACGG CCACCTATTA
        CACCACGACT GATACTGGTT GTACCTGGGC CACCTATGCC GGTGGATAAT

        BssHII                                          StyI
     ~~~~~~                                          ~~~~~
1101    TTGCGCGCGT TCTCCTCGTT ATCGTGGTGC TTTTGATTAT TGGGGCCAAG
        AACGCGCGCA AGAGGAGCAA TAGCACCACG AAAACTAATA ACCCCGGTTC

                            BlpI
```

```
                                       ~~~~~~~~
          StyI                         CelII
          ~
1151  GCACCCTGGT GACGGTTAGC TCAGCGTCGA CCAAAGGTCC AAGCGTGTTT
      CGTGGGACCA CTGCCAATCG AGTCGCAGCT GGTTTCCAGG TTCGCACAAA

1201  CCGCTGGCTC CGAGCAGCAA AAGCACCAGC GGCGGCACGG CTGCCCTGGG
      GGCGACCGAG GCTCGTCGTT TTCGTGGTCG CCGCCGTGCC GACGGGACCC

1251  CTGCCTGGTT AAAGATTATT TCCCGGAACC AGTCACCGTG AGCTGGAACA
      GACGGACCAA TTTCTAATAA AGGGCCTTGG TCAGTGGCAC TCGACCTTGT

1301  GCGGGGCGCT GACCAGCGGC GTGCATACCT TTCCGGCGGT GCTGCAAAGC
      CGCCCCGCGA CTGGTCGCCG CACGTATGGA AAGGCCGCCA CGACGTTTCG

1351  AGCGGCCTGT ATAGCCTGAG CAGCGTTGTG ACCGTGCCGA GCAGCAGCTT
      TCGCCGGACA TATCGGACTC GTCGCAACAC TGGCACGGCT CGTCGTCGAA

1401  AGGCACTCAG ACCTATATTT GCAACGTGAA CCATAAACCG AGCAACACCA
      TCCGTGAGTC TGGATATAAA CGTTGCACTT GGTATTTGGC TCGTTGTGGT

                                       EcoRI
                                       ~~~~~~~
1451  AAGTGGATAA AAAAGTGGAA CCGAAAAGCG AATTCGGGGG AGGGAGCGGG
      TTCACCTATT TTTTCACCTT GGCTTTTCGC TTAAGCCCCC TCCCTCGCCC

1501  AGCGGTGATT TTGATTATGA AAAGATGGCA AACGCTAATA AGGGGGCTAT
      TCGCCACTAA AACTAATACT TTTCTACCGT TTGCGATTAT TCCCCCGATA
                                    gIIIseq9   100.0%
                              ====================
1551  GACCGAAAAT GCCGATGAAA ACGCGCTACA GTCTGACGCT AAAGGCAAAC
      CTGGCTTTTA CGGCTACTTT TGCGCGATGT CAGACTGCGA TTTCCGTTTG

                                       ClaI
                                       ~~~~~~
1601  TTGATTCTGT CGCTACTGAT TACGGTGCTG CTATCGATGG TTTCATTGGT
      AACTAAGACA GCGATGACTA ATGCCACGAC GATAGCTACC AAAGTAACCA

1651  GACGTTTCCG GCCTTGCTAA TGGTAATGGT GCTACTGGTG ATTTTGCTGG
      CTGCAAAGGC CGGAACGATT ACCATTACCA CGATGACCAC TAAAACGACC

1701  CTCTAATTCC CAAATGGCTC AAGTCGGTGA CGGTGATAAT TCACCTTTAA
      GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGAAATT

1751  TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTTGAATGT
      ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1801  CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG
      GCGGGAAAAC AGAAACCGCG ACCATTTGGT ATACTTAAAA GATAACTAAC

1851  TGACAAAATA AACTTATTCC GTGGTGTCTT TGCGTTTCTT TTATATGTTG
      ACTGTTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1901  CCACCTTTAT GTATGTATTT TCTACGTTTG CTAACATACT GCGTAATAAG
      GGTGGAAATA CATACATAAA AGATGCAAAC GATTGTATGA CGCATTATTC
```

HindIII
~~~~~~
```
1951   GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
       CTCAGAACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                            OGIII3   100.0%
                            ====================
```

```
2001   ACATTTTTTT TGTCTGCCGT TTAATGAAAT TGTAAACGTT AATATTTTGT
       TGTAAAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA
```

```
2051   TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG
       ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC
```

```
2101   GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
       CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC
```

```
2151   GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
       CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC
```

```
2201   ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
       TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT
```

```
2251   CGAGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT GCCGTAAAGC
       GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG
```

```
2301   ACTAAATCGG AACCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
       TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCCTT
```

```
2351   AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC
       TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCG
```

```
2401   GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC
       CGATCCCGCG ACCGTTCACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG
```

```
2451   CGCCGCGCTT AATGCCGCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA
       GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT ACACTCGTTT
```

```
2501   AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT
       TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA
```

```
2551   TCCATAGGCT CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT
       AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA
```

```
2601   CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC
       GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG
```

```
2651   TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT
       ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA
```

```
2701   ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA
       TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT
```

```
2751   CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG
       GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC
```

ApaLI
~~~~~~

```
2801  TGTGCACGAA  CCCCCCGTTC  AGTCCGACCG  CTGCGCCTTA  TCCGGTAACT
      ACACGTGCTT  GGGGGGCAAG  TCAGGCTGGC  GACGCGGAAT  AGGCCATTGA

2851  ATCGTCTTGA  GTCCAACCCG  GTAAGACACG  ACTTATCGCC  ACTGGCAGCA
      TAGCAGAACT  CAGGTTGGGC  CATTCTGTGC  TGAATAGCGG  TGACCGTCGT

2901  GCCACTGGTA  ACAGGATTAG  CAGAGCGAGG  TATGTAGGCG  GTGCTACAGA
      CGGTGACCAT  TGTCCTAATC  GTCTCGCTCC  ATACATCCGC  CACGATGTCT

2951  GTTCTTGAAG  TGGTGGCCTA  ACTACGGCTA  CACTAGAAGA  ACAGTATTTG
      CAAGAACTTC  ACCACCGGAT  TGATGCCGAT  GTGATCTTCT  TGTCATAAAC

3001  GTATCTGCGC  TCTGCTGTAG  CCAGTTACCT  TCGGAAAAAG  AGTTGGTAGC
      CATAGACGCG  AGACGACATC  GGTCAATGGA  AGCCTTTTTC  TCAACCATCG

3051  TCTTGATCCG  GCAAACAAAC  CACCGCTGGT  AGCGGTGGTT  TTTTTGTTTG
      AGAACTAGGC  CGTTTGTTTG  GTGGCGACCA  TCGCCACCAA  AAAAACAAAC

3101  CAAGCAGCAG  ATTACGCGCA  GAAAAAAAGG  ATCTCAAGAA  GATCCTTTGA
      GTTCGTCGTC  TAATGCGCGT  CTTTTTTTCC  TAGAGTTCTT  CTAGGAAACT

3151  TCTTTTCTAC  GGGGTCTGAC  GCTCAGTGGA  ACGAAAACTC  ACGTTAAGGG
      AGAAAAGATG  CCCCAGACTG  CGAGTCACCT  TGCTTTTGAG  TGCAATTCCC

3201  ATTTTGGTCA  GATCTAGCAC  CAGGCGTTTA  AGGGCACCAA  TAACTGCCTT
      TAAAACCAGT  CTAGATCGTG  GTCCGCAAAT  TCCCGTGGTT  ATTGACGGAA

3251  AAAAAAATTA  CGCCCCGCCC  TGCCACTCAT  CGCAGTACTG  TTGTAATTCA
      TTTTTTTAAT  GCGGGGCGGG  ACGGTGAGTA  GCGTCATGAC  AACATTAAGT

3301  TTAAGCATTC  TGCCGACATG  GAAGCCATCA  CAAACGGCAT  GATGAACCTG
      AATTCGTAAG  ACGGCTGTAC  CTTCGGTAGT  GTTTGCCGTA  CTACTTGGAC

3351  AATCGCCAGC  GGCATCAGCA  CCTTGTCGCC  TTGCGTATAA  TATTTGCCCA
      TTAGCGGTCG  CCGTAGTCGT  GGAACAGCGG  AACGCATATT  ATAAACGGGT

3401  TAGTGAAAAC  GGGGGCGAAG  AAGTTGTCCA  TATTGGCTAC  GTTTAAATCA
      ATCACTTTTG  CCCCCGCTTC  TTCAACAGGT  ATAACCGATG  CAAATTTAGT

3451  AAACTGGTGA  AACTCACCCA  GGGATTGGCT  GAGACGAAAA  ACATATTCTC
      TTTGACCACT  TTGAGTGGGT  CCCTAACCGA  CTCTGCTTTT  TGTATAAGAG

3501  AATAAACCCT  TTAGGGAAAT  AGGCCAGGTT  TTCACCGTAA  CACGCCACAT
      TTATTTGGGA  AATCCCTTTA  TCCGGTCCAA  AAGTGGCATT  GTGCGGTGTA

3551  CTTGCGAATA  TATGTGTAGA  AACTGCCGGA  AATCGTCGTG  GTATTCACTC
      GAACGCTTAT  ATACACATCT  TTGACGGCCT  TTAGCAGCAC  CATAAGTGAG

    +1
3601  CAGAGCGATG  AAAACGTTTC  AGTTTGCTCA  TGGAAAACGG  TGTAACAAGG
      GTCTCGCTAC  TTTTGCAAAG  TCAAACGAGT  ACCTTTTGCC  ACATTGTTCC

3651  GTGAACACTA  TCCCATATCA  CCAGCTCACC  GTCTTTCATT  GCCATACGGA
      CACTTGTGAT  AGGGTATAGT  GGTCGAGTGG  CAGAAAGTAA  CGGTATGCCT

3701  ACTCCGGGTG  AGCATTCATC  AGGCGGGCAA  GAATGTGAAT  AAAGGCCGGA
      TGAGGCCCAC  TCGTAAGTAG  TCCGCCCGTT  CTTACACTTA  TTTCCGGCCT
```

```
3751  TAAAACTTGT GCTTATTTTT CTTTACGGTC TTTAAAAAGG CCGTAATATC
      ATTTTGAACA CGAATAAAAA GAAATGCCAG AAATTTTTCC GGCATTATAG

3801  CAGCTGAACG GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT
      GTCGACTTGC CAGACCAATA TCCATGTAAC TCGTTGACTG ACTTTACGGA

3851  CAAAATGTTC TTTACGATGC CATTGGGATA TATCAACGGT GGTATATCCA
      GTTTTACAAG AAATGCTACG GTAACCCTAT ATAGTTGCCA CCATATAGGT

3901  GTGATTTTTT TCTCCATTTT AGCTTCCTTA GCTCCTGAAA ATCTCGATAA
      CACTAAAAAA AGAGGTAAAA TCGAAGGAAT CGAGGACTTT TAGAGCTATT

3951  CTCAAAAAAT ACGCCCGGTA GTGATCTTAT TTCATTATGG TGAAAGTTGG
      GAGTTTTTTA TGCGGGCCAT CACTAGAATA AAGTAATACC ACTTTCAACC

4001  AACCTCACCC GACGTCTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG
      TTGGAGTGGG CTGCAGATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC

4051  GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG
      CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

                M13 Reverse  primer 100.0%
                ==================
4101  ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATT
      TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAA
```

Figure 15

MS-GPC-1:

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARQYGHRGGFD
HWGQGTLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFNESVFGGGTKLTVL
G

MS-GPC-6

VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGS
GGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGYGRYSPDLW
GQGTLVTVSS

VL

DIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASS
RATGVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNLPFTFGQGTKVEIK
RT

MS-GPC-8

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARSPRYRGAFD
YWGQGTLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMPQAVFGGGTKLTVL
G

MS-GPC-10

VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARQLHYRGGFD
LWGQGTLVTVSS

VL

DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLTMGVFGGGTKLTVL
G

MS-GPC-8-6
VH
QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARSPRYRGAFD
YWGQGTLVTVSS
VL
DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFGGGTKLTVL
G

MS-GPC-8-10
VH
QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARSPRYRGAFD
YWGQGTLVTVSS
VL
DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVFGGGTKLTVL
G

MS-GPC-8-17
VH
QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARSPRYRGAFD
YWGQGTLVTVSS
VL
DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDFSVYVFGGGTKLTVL
G

MS-GPC-8-27
VH
QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARSPRYRGAFD
YWGQGTLVTVSS
VL
DIVLTQPPSVSGAPGQRVTISCSGSSSNIGSNYVSWYQQLPGTAPKLLIYDNNQ
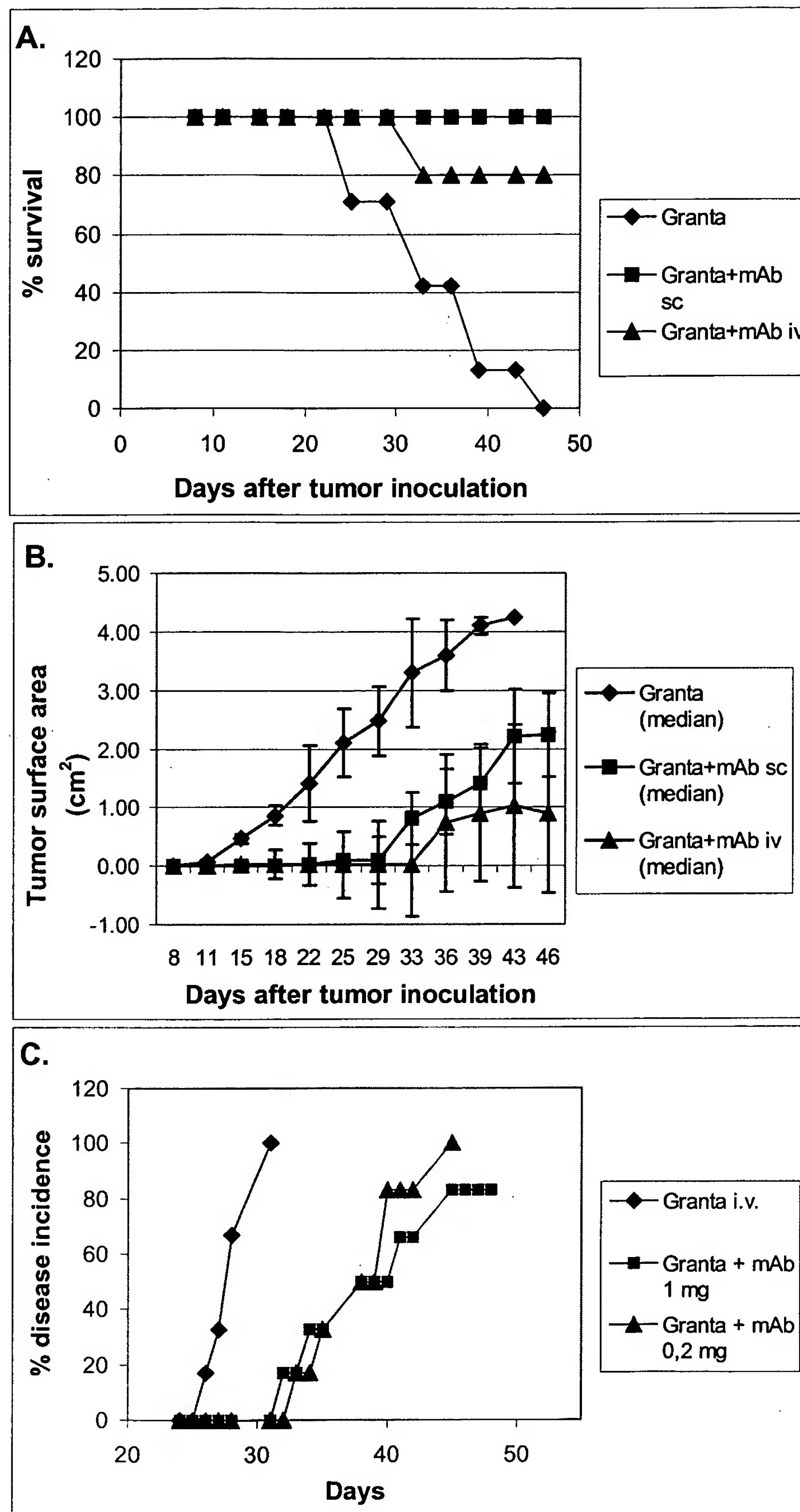RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHVFGGGTKLTVL
G

MS-GPC-8-6-13
VH

QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARSPRYRGAFD
YWGQGTLVTVSS
VL
DIVLTQPPSVSGAPGQRVTISCSGSESNIGANYVTWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDYDHYVFGGGTKLTVL
G

MS-GPC-8-10-57
VH
QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARSPRYRGAFD
YWGQGTLVTVSS
VL
DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVQWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDLIRHVFGGGTKLTVL
G

MS-GPC-8-27-41
VH
QVQLKESGPALVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALID
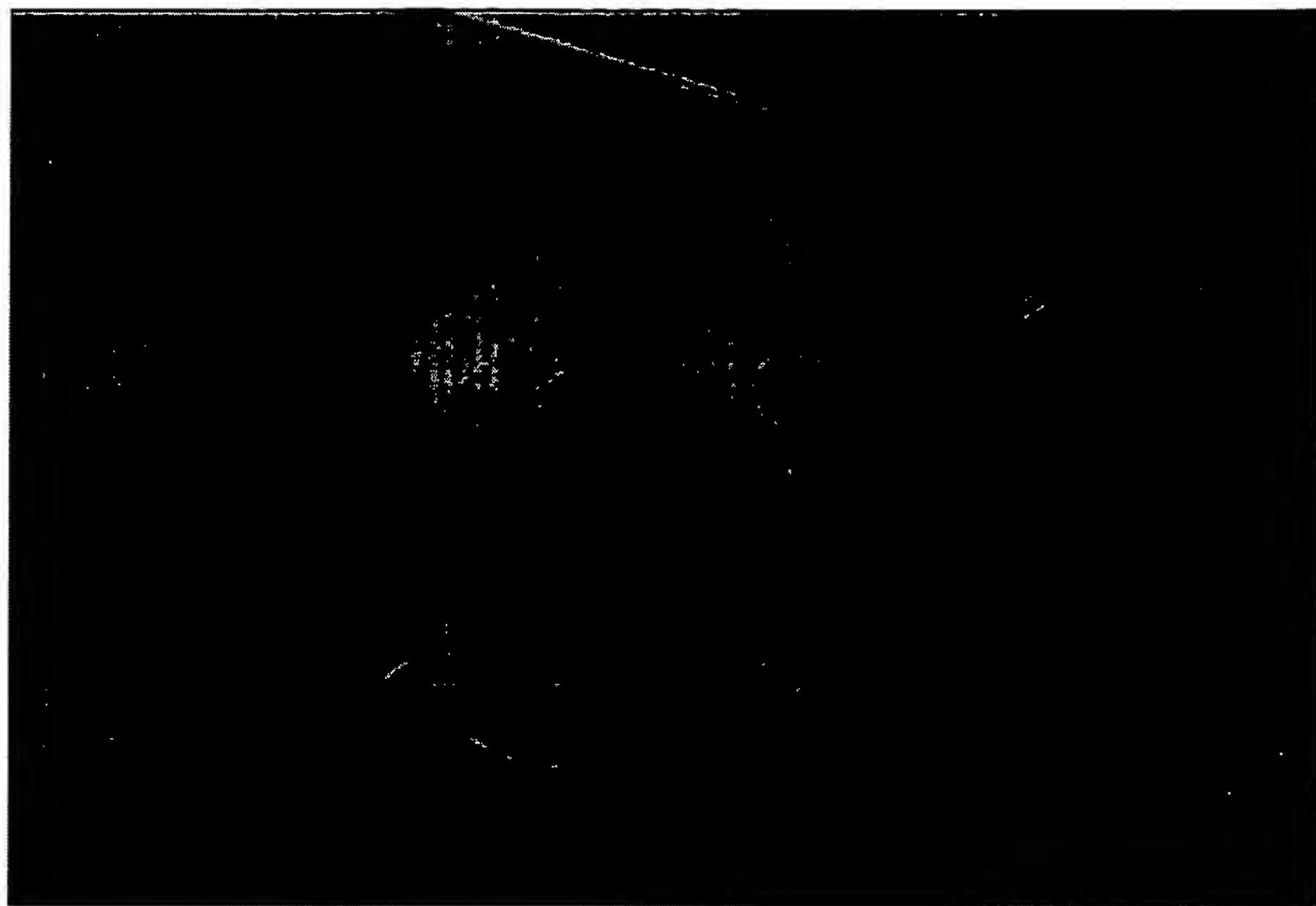WDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARSPRYRGAFD
YWGQGTLVTVSS
VL
DIVLTQPPSVSGAPGQRVTISCSGSESNIGNNYVQWYQQLPGTAPKLLIYDNNQ
RPSGVPDRFSGSKSGTSASLAITGLQSEDEADYYCQSYDMNVHVFGGGTKLTVL
G

Figure 16

Figure 16 (Cont.)

D

Mouse #2, untreated, day 32; tumor area 4.76 cm^2

E

Mouse #13, mAb i.v., day 32; tumor area 0.01 cm^2